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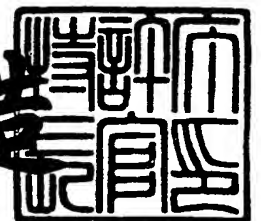
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【プルーフの要否】 要

【書類名】 明細書

【発明の名称】 分泌タンパク質、または膜タンパク質

【特許請求の範囲】

【請求項 1】 次の配列番号から選択される、いずれかの配列番号として記載されたアミノ酸配列からなる分泌タンパク質、または膜タンパク質。

配列番号：2、配列番号：4、配列番号：6、配列番号：8、配列番号：10、
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、配列番号：198、配列番号：200、配列番号：202、配列番号：204

、配列番号：2 0 6、配列番号：2 0 8、配列番号：2 1 0、配列番号：2 1 2
 、配列番号：2 1 4、配列番号：2 1 6、配列番号：2 1 8、配列番号：2 2 0
 、配列番号：2 2 2、配列番号：2 2 4、配列番号：2 2 6、配列番号：2 2 8
 、配列番号：2 3 0、配列番号：2 3 2、配列番号：2 3 4、配列番号：2 3 6
 、配列番号：2 3 8、配列番号：2 4 0、配列番号：2 4 2、配列番号：2 4 4
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 、配列番号：2 5 4、配列番号：2 5 6、配列番号：2 5 8、配列番号：2 6 0
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 、配列番号：3 2 6、配列番号：3 2 8、配列番号：3 3 0、配列番号：3 3 2
 、配列番号：3 3 4、および、配列番号：3 3 6

【請求項 2】請求項 1 に記載のいずれかのタンパク質をコードする DNA。

【請求項 3】次の配列番号から選択される、いずれかの配列番号として記載された塩基配列のコード領域からなる、請求項 2 に記載の DNA。

~~配列番号：1、配列番号：3、配列番号：5、配列番号：7、配列番号：9、配~~

列番号：1 1、配列番号：1 3、配列番号：1 5、配列番号：1 7、配列番号：
 1 9、配列番号：2 1、配列番号：2 3、配列番号：2 5、配列番号：2 7、配
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列番号：3 1 7、配列番号：3 1 9、配列番号：3 2 1、配列番号：3 2 3、配列番号：3 2 5、配列番号：3 2 7、配列番号：3 2 9、配列番号：3 3 1、配列番号：3 3 3、および配列番号：3 3 5

【請求項 4】請求項 2 または 3 に記載の DNA のいずれかが挿入されたベクター。

【請求項 5】請求項 2 または 3 に記載の DNA のいずれかを発現可能に保持する形質転換体。

【請求項 6】請求項 5 に記載の形質転換体を培養し、発現産物を回収する工程を含む、請求項 1 に記載の分泌タンパク質、または膜タンパク質のいずれかを製造する方法。

【請求項 7】請求項 2 または 3 に記載の DNA のいずれか、またはその相補鎖にハイブリダイズする DNA であって、少なくとも 1 5 ヌクレオチドの鎖長を持つ DNA。

【請求項 8】請求項 7 に記載の DNA からなる、分泌タンパク質、または膜タンパク質をコードするヒト全長 cDNA 合成用プライマー。

【請求項 9】請求項 7 に記載の DNA からなる、分泌タンパク質、または膜タンパク質をコードする遺伝子の検出用プローブ。

【請求項 1 0】請求項 2 または 3 に記載のいずれかの DNA もしくはその一部に対するアンチセンス DNA。

【請求項 1 1】次の工程を含む、ヒト分泌タンパク質、または膜タンパク質をコードする全長 cDNA の合成方法。

- a) cDNA ライブラリーを鋳型として請求項 8 に記載のプライマーを起点とする相補鎖合成反応を行い、
- b) 合成産物を回収する

【請求項 1 2】cDNA ライブラリーが、オリゴキャップ法によって合成されたものである請求項 1 1 に記載の合成方法。

【請求項 1 3】相補鎖の合成を PCR 法によって行う請求項 1 1 に記載の合成方法。

【請求項 1 4】請求項 1 に記載のいずれかのタンパク質に対する抗体。

【発明の詳細な説明】

【0001】

【発明の属する技術分野】

本発明は、ヒトに由来するタンパク質をコードする全長cDNA、このcDNAによってコードされるタンパク質、並びにそれらの製造および用途に関する。

【0002】

【従来の技術】

現在、世界的なレベルで様々な生物のゲノム配列の解明とその解析が進められている。既に10種類を越える原核微生物、下等真核生物の出芽酵母、多細胞性真核生物である線虫で、その全ゲノム配列が決定された。3,000,000,000塩基対といわれるヒトのゲノムについては、現在、世界的な協力体制のもとでその解析が進められており、2002～2003年頃までには、その全構造が明らかにされようとしている。ゲノム配列を明らかにする目的は、複雑な生命現象をその設計図であるゲノム情報を解読し、全ての遺伝子の機能や制御、あるいは遺伝子間、タンパク質間、細胞間さらには個体間における相互作用のネットワークとして生物を理解するところにある。種々の生物種のゲノム情報から生命現象を解明していくことは、単に学術分野における研究課題として重要であるのみならず、そこで得られる研究成果をいかに産業上の応用へと発展させていくかという点で、その社会的な意義も大きい。

ところが単にゲノム配列を決定しただけでは、全ての遺伝子の機能を明らかにできるわけではない。例えば酵母では、ゲノム配列から推定された約6,000の遺伝子の約半数しか、その機能を推定できなかった。一方、ヒトには約100,000種類の遺伝子が存在するといわれる。そこで、ゲノム配列から明らかにされてくる膨大な量の新しい遺伝子の機能を、迅速かつ効率的に解明していくための「ハイスループット遺伝子機能解析システム」の確立が、強く望まれている。

【0003】

真核生物のゲノム配列では、多くの場合、一つの遺伝子がイントロンによって複数のエキソンに分断されている。そのため、ゲノム配列情報だけからそこにコードされるタンパク質の構造を正確に予測するには、多くの問題がある。一方、

イントロンが除かれた mRNA から作製される cDNA では、タンパク質のアミノ酸配列の情報が一つの連続した配列情報として得られるため、容易にその一次構造を明らかにすることが可能である。ヒトの cDNA の研究では、これまでに 1,000,000 を越える EST (Expression Sequence Tags) データがパブリックドメインに公開されており、それらはヒトの全遺伝子の 80% 以上をカバーしているものと推定されている。

これらの情報は、ヒト遺伝子構造の解明やゲノム配列におけるエクソン領域の予測、あるいはその発現プロファイルの推定など、様々な角度から利用されている。ところが、これらのヒト EST 情報の多くは cDNA の 3' 末端側近傍に集中しているため、特に mRNA の 5' 末端近傍の情報が極端に不足している状況にある。また、これらのヒト cDNA の中でコードされているタンパク質の配列が予測されている mRNA は約 7,000 種類程度であり、更にそのうち全長 cDNA クローンとして取得されているものはわずか 5,500 種類程度に過ぎないのが現状である。EST として登録されているものを含めても、全長クローンとしてこれまでに取得されているヒト cDNA は、ヒト全遺伝子のわずかに 10%~15% 程度であると推定されている。

【0004】

完全長 cDNA では、その 5' 末端配列からゲノム配列上での mRNA 転写開始点が特定できる上、その配列の中に含まれる mRNA の安定性や翻訳段階での発現制御に関わる因子の解析が可能である。また、翻訳開始点である atg を 5' 側に含むことから、正しいフレームでタンパク質への翻訳を行うことができる。したがって、適当な遺伝子発現系を適用することで、その cDNA がコードするタンパク質を大量に

生産したり、タンパク質を発現させてその生物学的活性を解析することも可能になる。このように、完全長 cDNA の解析からはゲノム配列解析を相補する重要な情報が得られる。また、発現可能な全長 cDNA クローンは、その遺伝子の機能の実証的な解析や産業分野での応用への展開において、その重要性はきわめて高い。

【0005】

全長 cDNA を合成する方法は公知である。たとえばオリゴキャップ法 [K. Maruyama and S. Sugano, Gene, 138: 171-174 (1994); Y. Suzuki et al., Gene, 200: 149-156 (1997)] によれば、原理的には全長 cDNA に富むライブラリーを合成す

ることができる。合成したcDNAをクローニングし、その塩基配列を決定すれば、ATGpr [A. A. Salamov, T. Nishikawa, M. B. Swindells, Bioinformatics, 14: 384-390 (1998); <http://www.hri.co.jp/atgpr/>]等の手法を用いて、それが全長cDNAクローンであるかどうかを評価することができる。しかし、これら公知の手法の組み合わせでは、確かにある程度の割合で全長cDNAを得ることができるものの、その効率においては改善の余地を残していた。そのため、発現頻度の低いmRNAについては、その全長cDNAをクローニングすることは依然として困難なことと考えられている。

【0006】

特にヒト分泌タンパク質、または膜タンパク質には、そのものがTissue plasminogen activator (TPA)のように、医薬品として有用なものや、膜レセプターのように医薬品の標的タンパク質になりうるものが多い。

したがって、ヒトにおいて分離が進んでいない新規な全長cDNAを提供する意義は大きい。中でも、分泌タンパク質、または膜タンパク質をコードするcDNAは、タンパク質自身に医薬品としての有用性を期待できること、あるいは疾患に関連する遺伝子を多く含む可能性のあることから、未知のcDNAの分離が望まれている。したがって、これらのタンパク質をコードするcDNAの全長を明らかにすることには大きな意義がある。

【0007】

【発明が解決しようとする課題】

本発明は、ヒト由来の新規な分泌タンパク質、または膜タンパク質と、それをコードするDNA、並びにそれらの用途の提供を課題としている。

【0008】

【課題を解決するための手段】

我々は、オリゴキャップ法 [K. Maruyama and S. Sugano, Gene, 138: 171-174 (1994); Y. Suzuki et al., Gene, 200: 149-156 (1997)]で作成した全長率の高いヒトcDNAライブラリーから、ATGpr等で全長cDNAクローンであると予測される、ヒト全長cDNAを効率よくクローニングする方法を開発した。次いで、この方法で取得した全長率の高いcDNAクローンの塩基配列を5'側と3'側の両側から決定

した。こうして得られた塩基配列を利用し、PSORT [K. Nakai & M. Kanehisa, *Genomics*, 14: 897-911 (1992)] でシグナル配列を持つと予測されるクローンを特異的に選別し、分泌タンパク質、または膜タンパク質をコードするcDNAを有すると予測されるクローンを取得した。

本発明における全長cDNAクローンは、[1] オリゴキャップ法による全長率の高いcDNAライブラリーの作成、および[2] 5' 末端側の配列からの全長性の評価システムとの組み合わせによって取得することができた、より全長である確率の高いクローンである。

更に、この方法で取得したクローンの全長cDNA配列を解析し、その塩基配列がコードするアミノ酸配列を推定した。そして推定アミノ酸配列に基づいて、BLAST [S. F. Altschul, W. Gish, W. Miller, E. W. Myers & D. J. Lipman, *J. Mol. Biol.*, 215: 403-410 (1990); W. Gish & D. J. States, *Nature Genet.*, 3: 266-272 (1993); <http://www.ncbi.nlm.nih.gov/BLAST/>] によりGenBank (<http://www.ncbi.nlm.nih.gov/Web/Genbank/index.html>) やSwissProt (http://www.ebi.ac.uk/ebi_docs/swissprot_db/swisshome.html) を利用して相同性解析を行い、推定アミノ酸配列を持つタンパク質に予測される機能を明らかにして本発明を完成した。

【 0 0 0 9 】

すなわち本発明は、以下の分泌タンパク質、または膜タンパク質、このタンパク質をコードするDNA、並びにそれらの用途に関する。

まず本発明は、〔1〕表1に記載した配列番号から選択される、いずれかの配列番号として記載されたアミノ酸配列からなる分泌タンパク質、または膜タンパク質に関する。また本発明は、〔2〕〔1〕に記載のいずれかのタンパク質をコードするDNAに関する。本発明によるDNAの塩基配列は、たとえば〔3〕表1に記載の配列番号から選択される、いずれかの配列番号として記載された塩基配列のコード領域からなる。表1に、本発明による全長cDNAを有する実施例で単離したcDNAクローンの名称と、そのcDNAの塩基配列を表す配列番号、ならびにcDNAの塩基配列から推定されるアミノ酸配列を記載した配列番号の対応をまとめた。

【 0 0 1 0 】

【表 1】

アミノ酸配列	塩基配列	クローン名
配列番号 : 2	配列番号 : 1	PSEC0001
配列番号 : 4	配列番号 : 3	PSEC0004
配列番号 : 6	配列番号 : 5	PSEC0005
配列番号 : 8	配列番号 : 7	PSEC0007
配列番号 : 1 0	配列番号 : 9	PSEC0008
配列番号 : 1 2	配列番号 : 1 1	PSEC0012
配列番号 : 1 4	配列番号 : 1 3	PSEC0017
配列番号 : 1 6	配列番号 : 1 5	PSEC0019
配列番号 : 1 8	配列番号 : 1 7	PSEC0020
配列番号 : 2 0	配列番号 : 1 9	PSEC0021
配列番号 : 2 2	配列番号 : 2 1	PSEC0028
配列番号 : 2 4	配列番号 : 2 3	PSEC0029
配列番号 : 2 6	配列番号 : 2 5	PSEC0030
配列番号 : 2 8	配列番号 : 2 7	PSEC0031
配列番号 : 3 0	配列番号 : 2 9	PSEC0035
配列番号 : 3 2	配列番号 : 3 1	PSEC0038
配列番号 : 3 4	配列番号 : 3 3	PSEC0040
配列番号 : 3 6	配列番号 : 3 5	PSEC0041
配列番号 : 3 8	配列番号 : 3 7	PSEC0045
配列番号 : 4 0	配列番号 : 3 9	PSEC0048
配列番号 : 4 2	配列番号 : 4 1	PSEC0049
配列番号 : 4 4	配列番号 : 4 3	PSEC0051
配列番号 : 4 6	配列番号 : 4 5	PSEC0052
配列番号 : 4 8	配列番号 : 4 7	PSEC0053

配列番号：5 0	配列番号：4 9	PSEC0055
配列番号：5 2	配列番号：5 1	PSEC0059
配列番号：5 4	配列番号：5 3	PSEC0061
配列番号：5 6	配列番号：5 5	PSEC0068
配列番号：5 8	配列番号：5 7	PSEC0070
配列番号：6 0	配列番号：5 9	PSEC0071
配列番号：6 2	配列番号：6 1	PSEC0072
配列番号：6 4	配列番号：6 3	PSEC0073
配列番号：6 6	配列番号：6 5	PSEC0074
配列番号：6 8	配列番号：6 7	PSEC0075
配列番号：7 0	配列番号：6 9	PSEC0076
配列番号：7 2	配列番号：7 1	PSEC0077
配列番号：7 4	配列番号：7 3	PSEC0079
配列番号：7 6	配列番号：7 5	PSEC0080
配列番号：7 8	配列番号：7 7	PSEC0081
配列番号：8 0	配列番号：7 9	PSEC0082
配列番号：8 2	配列番号：8 1	PSEC0085
配列番号：8 4	配列番号：8 3	PSEC0086
配列番号：8 6	配列番号：8 5	PSEC0087
配列番号：8 8	配列番号：8 7	PSEC0088
配列番号：9 0	配列番号：8 9	PSEC0090
配列番号：9 2	配列番号：9 1	PSEC0094
配列番号：9 4	配列番号：9 3	PSEC0095
配列番号：9 6	配列番号：9 5	PSEC0098
配列番号：9 8	配列番号：9 7	PSEC0099
配列番号：1 0 0	配列番号：9 9	PSEC0100
配列番号：1 0 2	配列番号：1 0 1	PSEC0101
配列番号：1 0 4	配列番号：1 0 3	PSEC0104
配列番号：1 0 6	配列番号：1 0 5	PSEC0105

配列番号 : 1 0 8	配列番号 : 1 0 7	PSEC0106
配列番号 : 1 1 0	配列番号 : 1 0 9	PSEC0107
配列番号 : 1 1 2	配列番号 : 1 1 1	PSEC0108
配列番号 : 1 1 4	配列番号 : 1 1 3	PSEC0109
配列番号 : 1 1 6	配列番号 : 1 1 5	PSEC0110
配列番号 : 1 1 8	配列番号 : 1 1 7	PSEC0111
配列番号 : 1 2 0	配列番号 : 1 1 9	PSEC0112
配列番号 : 1 2 2	配列番号 : 1 2 1	PSEC0113
配列番号 : 1 2 4	配列番号 : 1 2 3	PSEC0119
配列番号 : 1 2 6	配列番号 : 1 2 5	PSEC0120
配列番号 : 1 2 8	配列番号 : 1 2 7	PSEC0121
配列番号 : 1 3 0	配列番号 : 1 2 9	PSEC0124
配列番号 : 1 3 2	配列番号 : 1 3 1	PSEC0125
配列番号 : 1 3 4	配列番号 : 1 3 3	PSEC0126
配列番号 : 1 3 6	配列番号 : 1 3 5	PSEC0127
配列番号 : 1 3 8	配列番号 : 1 3 7	PSEC0128
配列番号 : 1 4 0	配列番号 : 1 3 9	PSEC0129
配列番号 : 1 4 2	配列番号 : 1 4 1	PSEC0130
配列番号 : 1 4 4	配列番号 : 1 4 3	PSEC0131
配列番号 : 1 4 6	配列番号 : 1 4 5	PSEC0133
配列番号 : 1 4 8	配列番号 : 1 4 7	PSEC0134
配列番号 : 1 5 0	配列番号 : 1 4 9	PSEC0135
配列番号 : 1 5 2	配列番号 : 1 5 1	PSEC0136
配列番号 : 1 5 4	配列番号 : 1 5 3	PSEC0137
配列番号 : 1 5 6	配列番号 : 1 5 5	PSEC0139
配列番号 : 1 5 8	配列番号 : 1 5 7	PSEC0143
配列番号 : 1 6 0	配列番号 : 1 5 9	PSEC0144
配列番号 : 1 6 2	配列番号 : 1 6 1	PSEC0146
配列番号 : 1 6 4	配列番号 : 1 6 3	PSEC0147

配列番号：1 6 6	配列番号：1 6 5	PSEC0149
配列番号：1 6 8	配列番号：1 6 7	PSEC0150
配列番号：1 7 0	配列番号：1 6 9	PSEC0151
配列番号：1 7 2	配列番号：1 7 1	PSEC0152
配列番号：1 7 4	配列番号：1 7 3	PSEC0158
配列番号：1 7 6	配列番号：1 7 5	PSEC0159
配列番号：1 7 8	配列番号：1 7 7	PSEC0161
配列番号：1 8 0	配列番号：1 7 9	PSEC0162
配列番号：1 8 2	配列番号：1 8 1	PSEC0163
配列番号：1 8.4	配列番号：1 8 3	PSEC0164
配列番号：1 8 6	配列番号：1 8 5	PSEC0165
配列番号：1 8 8	配列番号：1 8 7	PSEC0167
配列番号：1 9 0	配列番号：1 8 9	PSEC0168
配列番号：1 9 2	配列番号：1 9 1	PSEC0169
配列番号：1 9 4	配列番号：1 9 3	PSEC0170
配列番号：1 9 6	配列番号：1 9 5	PSEC0171
配列番号：1 9 8	配列番号：1 9 7	PSEC0172
配列番号：2 0 0	配列番号：1 9 9	PSEC0173
配列番号：2 0 2	配列番号：2 0 1	PSEC0178
配列番号：2 0 4	配列番号：2 0 3	PSEC0181
配列番号：2 0.6	配列番号：2 0 5	PSEC0182

配列番号：2 0 8	配列番号：2 0 7	PSEC0183
配列番号：2 1 0	配列番号：2 0 9	PSEC0190
配列番号：2 1 2	配列番号：2 1 1	PSEC0191
配列番号：2 1 4	配列番号：2 1 3	PSEC0192
配列番号：2 1 6	配列番号：2 1 5	PSEC0197
配列番号：2 1 8	配列番号：2 1 7	PSEC0198
配列番号：2 2 0	配列番号：2 1 9	PSEC0199
配列番号：2 2 2	配列番号：2 2 1	PSEC0200

配列番号 : 2 2 4	配列番号 : 2 2 3	PSEC0203
配列番号 : 2 2 6	配列番号 : 2 2 5	PSEC0204
配列番号 : 2 2 8	配列番号 : 2 2 7	PSEC0205
配列番号 : 2 3 0	配列番号 : 2 2 9	PSEC0207
配列番号 : 2 3 2	配列番号 : 2 3 1	PSEC0209
配列番号 : 2 3 4	配列番号 : 2 3 3	PSEC0210
配列番号 : 2 3 6	配列番号 : 2 3 5	PSEC0213
配列番号 : 2 3 8	配列番号 : 2 3 7	PSEC0214
配列番号 : 2 4 0	配列番号 : 2 3 9	PSEC0215
配列番号 : 2 4 2	配列番号 : 2 4 1	PSEC0216
配列番号 : 2 4 4	配列番号 : 2 4 3	PSEC0218
配列番号 : 2 4 6	配列番号 : 2 4 5	PSEC0220
配列番号 : 2 4 8	配列番号 : 2 4 7	PSEC0222
配列番号 : 2 5 0	配列番号 : 2 4 9	PSEC0223
配列番号 : 2 5 2	配列番号 : 2 5 1	PSEC0224
配列番号 : 2 5 4	配列番号 : 2 5 3	PSEC0226
配列番号 : 2 5 6	配列番号 : 2 5 5	PSEC0227
配列番号 : 2 5 8	配列番号 : 2 5 7	PSEC0228
配列番号 : 2 6 0	配列番号 : 2 5 9	PSEC0230
配列番号 : 2 6 2	配列番号 : 2 6 1	PSEC0232
配列番号 : 2 6 4	配列番号 : 2 6 3	PSEC0233
配列番号 : 2 6 6	配列番号 : 2 6 5	PSEC0235
配列番号 : 2 6 8	配列番号 : 2 6 7	PSEC0236
配列番号 : 2 7 0	配列番号 : 2 6 9	PSEC0240
配列番号 : 2 7 2	配列番号 : 2 7 1	PSEC0241
配列番号 : 2 7 4	配列番号 : 2 7 3	PSEC0243
配列番号 : 2 7 6	配列番号 : 2 7 5	PSEC0244
配列番号 : 2 7 8	配列番号 : 2 7 7	PSEC0245
配列番号 : 2 8 0	配列番号 : 2 7 9	PSEC0246

配列番号：2 8 2 配列番号：2 8 1 PSEC0247

配列番号：2 8 4 配列番号：2 8 3 PSEC0248

配列番号：2 8 6 配列番号：2 8 5 PSEC0249

配列番号：2 8 8 配列番号：2 8 7 PSEC0250

配列番号：2 9 0 配列番号：2 8 9 PSEC0252

配列番号：2 9 2 配列番号：2 9 1 PSEC0253

配列番号：2 9 4 配列番号：2 9 3 PSEC0255

配列番号：2 9 6 配列番号：2 9 5 PSEC0258

配列番号：2 9 8 配列番号：2 9 7 PSEC0259

配列番号：3 0 0 配列番号：2 9 9 PSEC0260

配列番号：3 0 2 配列番号：3 0 1 PSEC0261

配列番号：3 0 4 配列番号：3 0 3 PSEC0263

配列番号：3 0 6 配列番号：3 0 5 PSEC0027

配列番号：3 0 8 配列番号：3 0 7 PSEC0047

配列番号：3 1 0 配列番号：3 0 9 PSEC0066

配列番号：3 1 2 配列番号：3 1 1 PSEC0067

配列番号：3 1 4 配列番号：3 1 3 PSEC0069

配列番号：3 1 6 配列番号：3 1 5 PSEC0092

配列番号：3 1 8 配列番号：3 1 7 PSEC0103

配列番号：3 2 0 配列番号：3 1 9 PSEC0117

配列番号：3 2 2 配列番号：3 2 1 PSEC0142

配列番号：3 2 4 配列番号：3 2 3 PSEC0212

配列番号：3 2 6 配列番号：3 2 5 PSEC0239

配列番号：3 2 8 配列番号：3 2 7 PSEC0242

配列番号：3 3 0 配列番号：3 2 9 PSEC0251

配列番号：3 3 2 配列番号：3 3 1 PSEC0256

配列番号：3 3 4 配列番号：3 3 3 PSEC0195

配列番号：3 3 6 配列番号：3 3 5 PSEC0206

【0011】

更に本発明は、上記タンパク質やDNAに基づく以下の用途に関する。

〔4〕〔2〕または〔3〕に記載のDNAのいずれかが挿入されたベクター。

〔5〕〔2〕または〔3〕に記載のDNAのいずれかを発現可能に保持する形質転換体。

〔6〕〔5〕に記載の形質転換体を培養し、発現産物を回収する工程を含む、〔1〕に記載の分泌タンパク質、または膜タンパク質のいずれかを製造する方法。

〔7〕〔2〕または〔3〕に記載のDNAのいずれか、またはその相補鎖にハイブリダイズするDNAであって、少なくとも15ヌクレオチドの鎖長を持つDNA。

〔8〕〔7〕に記載のDNAからなる、分泌タンパク質、または膜タンパク質をコードするヒト全長cDNA合成用プライマー。

〔9〕〔7〕に記載のDNAからなる、分泌タンパク質、または膜タンパク質をコードする遺伝子の検出用プローブ。

〔10〕〔2〕または〔3〕に記載のいずれかのDNAもしくはその一部に対するアンチセンスDNA。

〔11〕次の工程を含む、ヒト分泌タンパク質、または膜タンパク質をコードする全長cDNAの合成方法。

a) cDNAライブラリーを鋳型として〔8〕に記載のプライマーを起点とする相補鎖合成反応を行い、

b) 合成産物を回収する

〔12〕cDNAライブラリーが、オリゴキャップ法によって合成されたもので

ある〔11〕に記載の合成方法。

〔13〕相補鎖の合成をPCR法によって行う〔11〕に記載の合成方法。

〔14〕〔1〕に記載のいずれかのタンパク質に対する抗体。

【0012】

本発明において、ポリヌクレオチドとはヌクレオチドが多数重合した分子を意味する。重合するヌクレオチドの数は特に制限されないが、比較的重合度の低い場合には特にオリゴヌクレオチドとも表現する。本発明のポリヌクレオチド、またはオリゴヌクレオチドは、天然のものであることもできるし、化学的に合成さ

れたものであることもできる。あるいはまた、鋳型となるDNAをもとにPCRのような酵素的な反応によって合成されたものであっても良い。

本発明によって提供されるcDNAはいずれも全長cDNAである。本発明における全長cDNAとは、そのcDNAの翻訳開始点となるATGコドンと終止コドンを備えたcDNAを意味する。したがって、天然のmRNAがタンパク質コード領域の上流や下流に本来備えている非翻訳領域の有無は問わない。

【0013】

【発明の実施の形態】

本発明は、表1に示すように配列番号：2～配列番号：336の偶数番号のアミノ酸配列のいずれかがからなる、ヒト由来の分泌タンパク質、または膜タンパク質である。本発明による168種のタンパク質のうち152種は、表2～表8に示すようなcDNAクローンによってコードされている。これらのクローンは、「全長率の高いオリゴキャップ法で作成したヒトcDNAライブラリーから、ATGpr等で全長cDNAクローンであると予測され、かつ、PSORTでN末端にシグナル配列が存在する分泌タンパク質、または膜タンパク質と予測されるクローン」であった。

【0014】

【表 2】

クローン番号	cDNA サイズ (bp)	アミノ 酸	ATG No.	ATGpr1	アノテーション
PSEC0001	1992	226	1	0.94	402/648 (62%) similarity to mouse Golgi 4-transmembrane transporter mRNA
PSEC0004	1883	326	1	0.94	532/852 (62%) similarity to human death effector domain-containing testicular molecule mRNA
PSEC0005	1366	220	1	0.94	430/592 (72%) similarity to human hCPE-R mRNA for CPE-receptor
PSEC0007	3425	570	1	0.94	1578/1580 (99%) similarity to human FK506-binding protein (FKBP63) mRNA, partial cds.
PSEC0008	978	215	1	0.94	44/119 (36%) aa identity to fission yeast hypothetical 72.5 kD protein C2F7.10 in chr. I
PSEC0012	1499	183	1	0.82	125/183 (68.3%) aa identity to fugu putative protein 2 (PUT2).
PSEC0017	3125	273	1	0.33	467/680 (68%) similarity to human placenta (Diff33) mRNA.
PSEC0019	1927	339	1	0.90	No similarity
PSEC0020	1483	393	1	0.69	No similarity
PSEC0021	1851	116	3	0.20	208/277 (75%) similarity to rabbit alpha-1-globin gene to theta-1-globin pseudogene region.
PSEC0028	2395	348	2	0.56	335/933 (68%) similarity to human GP36b glycoprotein mRNA
PSEC0029	1683	300	1	0.90	58/187 (31%) aa identity to Klebsiella terrigena acetoin(diacetyl) reductase (acetoin dehydrogenase)
PSEC0030	1584	406	1	0.26	No similarity
PSEC0031	1336	136	2	0.20	No similarity
PSEC0035	1729	406	1	0.93	36/127 (28%) aa identity to bull frog olfactomedin precursor (olfactory mucus protein)
PSEC0038	1883	223	1	0.90	No similarity
PSEC0040	2027	216	2	0.82	1538/1539 (99%) similarity to human cosmid 398G5 from a region of the tip of the short arm of chr.16.
PSEC0041	2518	240	2	0.51	No similarity
PSEC0045	1631	372	1	0.85	256/258 (99%) similarity to human KIA0384 gene
PSEC0048	3707	383	2	0.71	32/100 (32%) aa identity to Bacillus licheniformis glutamyl endopeptidase precursor (glutamate specific endopeptidase)
PSEC0049	2652	131	1	0.35	46/126 (36%) aa identity to baker's yeast hypothetical 15.7kD protein in NUP85-SSC1 intergenic region
PSEC0051	3293	227	3	0.63	62/224 (27%) aa identity to E. coli hypothetical protein in XAPB-LIG intergenic region (fragment)

(注 1) すべてのクローンのORFのN末にシグナル配列が存在する。

(注 2) PSEC0017, PSEC0030 & PSEC0031 : 5'-未配列が、すべてGenBankのdbESTの配列よりも長い。

(注 3) PSEC0049 : ORFの5'-未配列が、GenBankのdbESTの配列よりも長い。

1 / 7 (続きあり)

【0015】

【表 3】

PSEC0052	3635	578	2	0.94	127/348 (36%) aa identity to <i>Thermus aquaticus</i> aqualysin-1 precursor (serin protease).
PSEC0053	2366	285	1	0.94	59/162 (36%) aa identity to human collagen alpha a(VII) chain precursor (long-chain collagen)
PSEC0055	2147	331	2	0.92	99/318 (31%) aa identity to baker's yeast hypothetical 39.3KD protein in GCN4-WBP1 intergenic region.
PSEC0059	2863	230	3	0.72	388/643 (60%) similarity to mouse mCPE-R mRNA for CPE receptor
PSEC0061	1931	464	1	0.94	128/356 (35%) aa identity to baker's yeast beta-mannosyltransferase.
PSEC0068	1717	194	1	0.64	No similarity
PSEC0070	2510	286	3	0.94	540/804 (67%) similarity to mouse integral membrane protein 1 (Itm1) mRNA
PSEC0071	3558	875	1	0.94	278/762 (36%) aa identity to human inter-alpha-trypsin inhibitor complex component II precursor
PSEC0072	2092	350	1	0.94	No similarity
PSEC0073	2341	523	1	0.94	174/477 (36%) aa identity to rabbit UDP-glucuronosyltransferase microsomal (UDPGT) (fragment)
PSEC0074	2971	770	1	0.89	1620/1839 (88%) similarity to mouse semaphorin M mRNA, partial cds.
PSEC0075	2244	633	2	0.79	81/206 (39%) aa identity to baker's yeast hypothetical 139.1 KD protein C08B11.3 in chr.11.
PSEC0076	3253		1	0.94	56/194 (28%) aa identity to <i>Neurospora crassa</i> 72 kD mitochondrial outer membrane protein (mitochondrial import receptor for the ADP/ATP carrier)
PSEC0077	2195	860	1	0.94	34/120 (28%) aa identity to chicken troponin I, cardiac muscle isoforms
PSEC0079	1290	189	2	0.94	586/590 (99%) similarity to human Chr.4 BAC clone B366024
PSEC0080	3171	740	2	0.94	510/730 (69%) aa identity to human prostate specific membrane antigen.
PSEC0081	2890	172	1	0.94	114/178 (64%) similarity to mouse mRNA for DP5 that is involved in programmed cell death
PSEC0082	1878	331	1	0.94	93/269 (34%) aa identity to <i>Streptomyces antibioticus</i> probable oxidoreductase
PSEC0085	2392	280	1	0.85	No similarity
PSEC0086	1821	390	1	0.83	58/210 (27%) identity to human normal cross-reacting antigen precursor (C066C); 62/237 (26%) aa identity to mouse biliary glycoprotein 1 precursor (BGP-1)

(注) すべてのクロードンのORFのN末にシグナル配列が存在する。

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【 0 0 1 6 】

【表 4】

PSEC0087	1808	441	1	349/636 (65%) similarity to human chr. 16 BAC clone CIT987SK-A-0.94/69G12, complete sequence
PSEC0088	2015	467	1	0.94/109/315 (34%) aa identical to bovine cathepsin B precursor.
PSEC0090	1722	543	1	0.92 No similarity
PSEC0094	2291	564	1	0.93/80/284 (28%) aa identity to baker's yeast protein PTM1 precursor
PSEC0095	2080	349	1	0.94/1207/1207 (100%) similarity to human DNA sequence from clone 97N18
PSEC0098	2185	208	1	791/1361 (58%) similarity to human zinc-finger DNA binding motifs (1A-1) mRNA
PSEC0099	1627	350	2	Weakly similar to C. elegans hypothetical 26.4 KD protein EEED8.8 in chr. 11
PSEC0100	1391	172	1	0.77 No similarity
PSEC0101	2547	258	2	66/189 (34%) aa identity to Streptomyces fradiae hypothetical 35.5 KD protein in transposon TN4556.
PSEC0104	1430	418	2	55/230 (23%) aa identity to Bacillus subtilis hypothetical 48.6 KD protein in SERZ-DNAZ intergenic region
PSEC0105	2506	494	1	0.94 No similarity
PSEC0106	2465		2	1160/1162 (99%) similarity to human 17-beta-hydroxysteroid dehydrogenase (EDH17B2) gene, complete cds; PSEC0106のORFは17-beta-hydroxysteroid dehydrogenaseとは異なる
PSEC0107	2557	130	2	0.89/2164/2182 (99%) similarity to human chromosome 9q34, clone 23B4
PSEC0108	3099	267	3	86/207 (28%) aa identity to fission yeast hypothetical 49.3KD protein in C30D11.06C in Chr. 1.
PSEC0109	2563	736	1	0.94/575/669 (66%) similarity to human unknown protein B mRNA
PSEC0110	2179	344	1	0.94 No similarity
PSEC0111	3362	208	1	0.83/44/115 (38%) aa identity to human mucin 3.
PSEC0112	3598	349	4	0.74 No similarity
PSEC0113	2451	423	1	924/1627 (56%) similarity to SC3F7.12 gene region (probable polyketide synthase) of Streptomyces coelicolor cosmid 3F7
PSEC0119	2518	555	1	0.87 No similarity
PSEC0120	2250	302	2	2065/2235 (92%) similarity to human alpha-1,3-mannosyl-glycoprotein beta-1, 2-N-acetylglucosaminyltransferase (MGAT) gene
PSEC0121	1666	358	1	0.94/76/174 (43%) aa identity to human DNA J protein homolog 2
PSEC0124	1686	476	1	0.91/45% similar to Aedes aegypti vitellogenin carboxypeptidase precursor
PSEC0125	1999	256	1	0.74 Weakly similar to mouse proline-rich protein MP-3.
PSEC0126	1906	102	1	838/970 (86%) similarity to human mRNA for leukotriene B4 omega-hydroxylase

(注) すべてのクロードンのORFのN末にシグナル配列が存在する。

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【0017】

【表 5】

PSEC0127	1773	218	1	0.94	No similarity	
PSEC0128	2134	306	1	0.94	53/236 (22%) aa identity similar to human biliary glycoprotein 1 precursor (antigen CD66).	
PSEC0129	1828	135	1	0.94	1564/1615 (96%) similarity to human chromosome 16q13/21 BAC clone C11987SK-A-152E5	
PSEC0130	2934	265	1	0.68	Weakly similar to mouse keratin, type 1 cytokeletal 10	
PSEC0131	1658	297	1	0.94	No similarity	
PSEC0133	2023	240	1	0.94	No similarity	
PSEC0134	1898	144	6	0.71	No similarity.	
PSEC0135	1755	322	3	0.75	52/163 (31%) aa identity to rat CD44 antigen precursor	
PSEC0136	1907	392	1	0.93	No similarity	
PSEC0137	2981	571	1	0.94	No similarity.	
PSEC0139	1361	218	2	0.89	255/299 (85%) similarity to human KIAA0395 mRNA.	
PSEC0143	1976	125	1	0.74	50/129 (38%) aa identity to baker's yeast endosomal p24A protein. precursor	
PSEC0144	2067	247	1	0.94	No similarity.	
PSEC0146	2807	346	7	0.79	98/315 (31%) Meleagris gallopavo P2Y purinoceptor 1 (ATP receptor)	
PSEC0147	1964	520	1	0.91	79/203 (38%) aa identity to C.elegance 52.8 kD protein T05E11.5 in chr. IV	
PSEC0149	1988	432	1	0.94	101/101(100%) similarity to human 90 kD heat shock protein gene	
PSEC0150	2259	217	1	0.94	379/615 (61%) similarity to human TBX2 (TBX2) mRNA	
PSEC0151	1688	467	1	0.93	254/459 (55%) aa identity to human tissue alpha-L-fucosidase precursor	
PSEC0152	2130	374	2	0.86	No similarity	
PSEC0158	1836	137	4	0.94	406/609 (66%) similarity to rat neural membrane protein 35 mRNA	
PSEC0159	2198	372	1	0.80	362/606 (59%) similarity to Streptomyces coelicolor cosmid 3F9.	
PSEC0161	2222	496	1	0.89	203/479 (42%) aa identity to human gulucose transporter type 5, small intestine (fructose transporter)	
PSEC0162	1320	271	1	0.83	No similarity.	
PSEC0163	2167	578	1	0.94	84/228 (36%) aa identity to baker's yeast hypothetical 67.8 kD protein in GND1-ERG9 intergenic region; 669/669 (100%) similarity to human DNA sequence from clone 453C12	
PSEC0164	1877	463	1	0.93	67/169 (39%) aa identity to human glioma pathogenesis-related protein	
PSEC0165	2111	242	1	0.83	1469/1489 (98%) identity to human Chr.11 cosmid cSRL16b6.	
PSEC0167	874	103	7	0.73	No similarity.	

(注) すべてのクローンの中のORFのN末にシグナル配列が存在する。

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【0018】

【表 6】

PSEC0168	2533	269	1	55/179 (30%) aa identity to baker's yeast 42.5kDa protein in TSM1-ARE1 intergenic region	0.94
PSEC0169	1792	204	1	49/201 (24%) aa identity to Schistosoma mansoni 23 kD integral membrane protein; 47/143 (32%) aa identity to mouse CD63 antigen	0.75
PSEC0170	2622	353	1	602/1052 (57%) similarity to human IGF binding protein complex acidic subunit a mRNA; 85/259 (32%) aa identity to human platelet glycoprotein V precursor	0.94
PSEC0171	2005	301	2	No similarity.	0.91
PSEC0172	2012	415	1	546/869 (62%) similarity to human mRNA for type 1 procollagen C-proteinase enhancer protein; 77/233 (33%) aa identity to Xenopus laevis bone morphogenetic protein 1 precursor	0.92
PSEC0173	1740	406	1	191/306 (62%) similarity to rat calcium-independent alpha-latrotoxin receptor mRNA.	0.91
PSEC0178	2308	222	3	No similarity.	0.94
PSEC0181	1890	165	3	No similarity.	0.66
PSEC0182	2153	657	2	217/507 (42%) aa identity to human polypeptide N-acetyl-galactosaminyltransferase (GALNAC-T1)	0.82
PSEC0183	2031	451	1	1252/1526 (82%) similarity to mouse matrilin-2 mRNA; 113/230 (49%) aa identity to human cartilage matrix protein precursor	0.88
PSEC0190	1841	194	1	No similarity.	0.87
PSEC0191	1493	472	1	740/959 (77%) similarity to human elastin mRNA; 248/367 (67%) aa identity to human elastin precursor (tropoelastin)	0.87
PSEC0192	1557	153	1	1198/1203 (99%) similarity to human chromosome 5, BAC clone 8e5 (LBNL H167)	0.93
PSEC0197	3555	576	2	55/169 (32%) aa identity to baker's yeast peroxisomal-coenzyme A synthase	0.85
PSEC0198	2083	343	1	28/106 (26%) aa identity to baker's yeast hypothetical 64.0 kD protein in MMS21-UBC8 intergenic region	0.94
PSEC0199	2586	283	1	No similarity.	0.94
PSEC0200	1548	443	1	0.94/95/328 (28%) aa identity to human poliovirus receptor precursor	0.94
PSEC0203	1457	323	1	No similarity.	0.87
PSEC0204	1484	142	1	1409/1418 (99%) similarity to human DNA from chromosome 19, cosmid R29144	0.74
PSEC0205	1656	435	1	96/290 (33%) aa identity to baker's yeast cell division control protein 91	0.94
PSEC0207	1754	262	3	No similarity.	0.94

(注) すべてのクローンの中のORFのN末にシグナル配列が存在する。

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【0 0 1 9】

【表 7】

PSEC0209	2144	186	1	0.93	No similarity	
PSEC0210	1689	349	1	0.71	No similarity	
PSEC0213	1824	323	1	0.94	No similarity	
PSEC0214	1959	141	1	0.94	No similarity	
PSEC0215	2112	551	2	0.94	67/177 (33%) aa identity to rat collagen alpha 1(I) chain	
PSEC0216	1765	410	2	0.89	583/1173 (58%) similarity to human alpha2-C4-adrenergic receptor gene	
PSEC0218	1369	242	1	0.69	379/619 (61%) similarity to human torsinA (DYT1) mRNA; 265/431 (61%) similarity to human torsinB (DQ1) mRNA	
PSEC0220	1584	365	1	0.94	354/365 (96%) aa identity to mouse WNT-6 protein precursor;	
PSEC0222	899	139	2	0.94	1084/1310 (82%) similarity to mouse Wnt-6 mRNA	
PSEC0223	1874	221	1	0.94	247/300 (82%) similarity to human mitochondrial RNA-processing endoribonuclease RNA (mrp) gene	
PSEC0224	1463	170	1	0.89	1051/1053 (99%) similarity to human chromosome 5, BAC clone 8e5 (LBNL H167)	
PSEC0226	2103	477	1	0.91	91/172 (52%) aa identity to human carboxypeptidase N precursor (arginine carboxypeptidase)	
PSEC0227	1410		2	0.81	1055/1095 (97%) similarity to human mRNA for KIAA0199 gene, partial cds; 925/1099 (84%) similarity to chinese hamster SREBP cleavage activating protein (SCAP) mRNA	
PSEC0228	1483	146	1	0.92	143/219 (65%) similarity to c.elegans F57B10; 32/89 (35%) aa identity to hamster cop-coated vesicle membrane protein P24.	
PSEC0230	1784	271	1	0.76	245/271 (90%) aa identity to mouse signal recognition particle receptor beta subunit; 720/854 (84%) similarity to mouse signal recognition particle receptor beta subunit mRNA	
PSEC0232	1709	246	1	0.75	70/195 (35%) aa identity to human complement C1Q subcomponent, c chain precursor	
PSEC0233	2499	267	1	0.82	317/324 (97%) similarity to human genomic DNA (chr. 3; clone N1106R)	
PSEC0235	1601	211	1	0.94	No similarity	
PSEC0236	1906	529	1	0.94	293/472 (62%) aa identity to human laminin gamma-1 chain precursor	
PSEC0240	1638	253	1	0.94	768/816 (94%) similarity to human mRNA for WNT11 gene; 199/220 (90%) aa identity to mouse WNT-11 protein precursor	

(注) すべてのクローンのORFのN末にシグナル配列が存在する。

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【 0 0 2 0 】

【表 8】

PSEC0241	3593	622	1	152/531 (28%) aa identity to human mucin1 precursor (polymorphic epithelial mucin); 1301/1862 (69%) similarity to human mRNA for KIAA0584 protein
PSEC0243	2835	743	3	0.85 KIAA0584 protein
PSEC0244	2063	287	1	0.77 334/345 (96%) similarity to CIT-HSP Human genomic clone 2335H8
PSEC0245	2896	418	3	0.91 No similarity
PSEC0246	2969	345	1	0.91 377/483 (78%) aa identity to rat integral membrane glycoprotein gp120 precursor
PSEC0247	2872	236	1	0.94 60/151 (39%) aa identity to human low-density lipoprotein receptor precursor
PSEC0248	2694	172	1	0.94 328/540 (60%) similarity to human Tspan-4 mRNA; 70/237 (29%) aa identity to human platelet-endothelial tetraspan antigen 3 (PETA-3)
PSEC0249	3320	534	1	0.84 2279/2368 (96%) similarity to genomic sequence from human 9q34.
PSEC0250	2179	223	2	0.94 75/243 (30%) aa identity to bovine butyrophilin precursor; 807/1455 (55%) similarity to mouse transcription factor USF2 (USF2) gene, exons 1-7
PSEC0252	2617	491	3	0.89 81/231 (35%) aa identity to Drosophila melanogaster twisted gastrulation protein precursor
PSEC0253	2872	265	1	0.74 748/755 (99%) similarity to human mRNA for eosinophil granule major basic protein (5'-non coding region of HEGMP)
PSEC0255	3774	687	2	0.91 910/1351 (67%) similarity to human phosphatidylinositol-4-phosphate 5 kinase type II beta mRNA; 143/240 (59%) aa identity to human phosphatidylinositol-4-phosphate 5 kinase type III
PSEC0258	3791	349	1	0.89 92/317 (29%) aa identity to human leucocyte antigen CD97 precursor
PSEC0259	2583	242	2	0.94 No similarity.
PSEC0260	2492	496	1	0.94 1613/1619 (99%) similarity to human chromosome 11q12 pac pDJ57114; 92/211 (43%) aa identity to human cytochrome b561
PSEC0261	3080	806	2	0.94 No similarity.
PSEC0263	4144	971	2	0.82 82/307 (26%) aa identity to baker's yeast glucose repression mediator protein; 41/175 (23%) aa identity to Neurospora crassa mitochondrial precursor proteins import receptor (72 kD mitochondrial outer membrane protein)
				0.76 3898/3911 (99%) similarity to human mRNA for KIAA0090 gene, partial cds [897/971 (92.3%) aa identity to KIAA0090 protein]; 135/553 (24%) aa identity to baker's yeast hypothetical 87.2kd protein in APA1/DTP-PPD11 intergenic region

(注) すべてのクローンのORFのN末にシグナル配列が存在する。

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【0 0 2 1】

(注1) ATGpr1の値がやや低いクローン (PSEC0017, ATGpr1 0.33; PSEC0030, ATGpr1 0.26; PSEC0031, ATGpr1 0.20; PSEC0049, ATGpr1 0.35) : これらのクローンは、5'-端配列データ (one pass sequencing) をATGprで選別はしておらず、5'-端配列データからシグナル配列をもち、かつ、5'-端配列データでのORFの長いものとして選別してきたクローンを全長cDNA配列解析したものである。こ

れらはすべてN-末端にシグナル配列が存在していた。また、以上4クローンのうちPSEC0049以外のものは、ESTとの比較の結果cDNAの5'末端側に長かった。またPSEC0049は、ESTと比較してcDNAのORFにおいて5'末端側に長かった。つまり、これらのクローンがいずれも全長cDNAであることが明らかである。

【0022】

一方、本発明による168種のタンパク質のうち次の14種は、表9に示すようなcDNAクローン (PSEC0027, PSEC0047, PSEC0066, PSEC0067, PSEC0069, PSEC0092, PSEC0103, PSEC0117, PSEC0142, PSEC0212, PSEC0239, PSEC0242, PSEC0251, PSEC0256) によってコードされている。これらのクローンは、5'-端配列データ (one pass sequencing) からは分泌タンパク質、または膜タンパク質と予測されながら、全長cDNA配列をPSORTで解析した結果は、N-末端にシグナル配列が存在しなかった。しかし、MEMSAT [D. T. Jones, W. R. Taylor & J. M. Thornton, Biochemistry, 33: 3038-3049 (1994)] での解析により膜タンパク質 (transmembrane helixをもつ) であると予測された。同様にこれら全てのクローンがSOSUI [T. Hirokawa et.al. Bioinformatics, 14, 378-379 (1998)] (三井情報開発株式会社販売) でも膜タンパク質であると予測された。すなわち、「全長率の高いオリゴキャップ法で作成したヒトcDNAライブラリーから、ATGpr等で全長cDNAクローンであると予測され、かつ、MEMSATとSOSUIで膜タンパク質と予測されるクローン」であった。これらのクローンによってコードされるタンパク質も上記分泌タンパク質、または膜タンパク質のカテゴリーに入れられる。これら14クローンのうちで2クローン (PSEC0242とPSEC0251) は、N-末端にシグナル配列をも

たない膜タンパク質と予測された。しかし、いずれのクローンも3番目のATG (ともにATGpr1の値が高い) から翻訳がはじまるとするとN-末端にシグナル配列が存在する。このため、これらの2クローンについては、N-末端にシグナル配列が存在する分泌タンパク質、または膜タンパク質のカテゴリーに入る可能性もある。

【0023】

【表 9】

クローン番号	サイズ (bp)	アミノ酸	ATG No.	ATGpr1	SP & MEMSAT	アノテーション
PSEC0027	1085	271	1	0.94	No & transmembrane	No similarity
PSEC0047	2048	267	1	0.94	No & transmembrane	No similarity
PSEC0066	2882	474	1	0.79	No & transmembrane	55/173 (31%) aa identity to E.coli tetracycline resistance protein, class E.
PSEC0067	2405	730	1	0.26	No & transmembrane	935/1603 (58%) similarity to mouse very-long-chain acyl-CoA synthase (VLCS)
PSEC0069	2568	433	2	0.94	No & transmembrane	151/459 (32%) aa identity to human collagen alpha 1(X) chain precursor
PSEC0092	3624	465	1	0.94	No & transmembrane	758/1057 (71%) similarity to human mRNA for heparan-sulfate 6-sulfotransferase
PSEC0103	2530	236	1	0.94	No & transmembrane	457/707 (64%) similarity to rat norvegicus RS-Rex-s mRNA
PSEC0117	1873	583	1		No & transmembrane	627/630 (99%) similarity to human DNA from chromosome 19-cosmid R30879 containing USF2, genomic sequence
PSEC0142	2153	343	2	0.94	No & transmembrane	291/343 (84%) aa identity to rat probable G protein-coupled receptor RTA
PSEC0212	1677	111	1	0.94	No & transmembrane	inflammatory protein-2-alpha (MIP2-alpha); 31/91 (34%) aa identity to human growth regulated protein precursor
PSEC0239	1712	423	2	0.18	No & transmembrane	88/231 (38%) aa identity to human progastricin (pepsinogen C).
PSEC0242	3017		1		No & transmembrane	242/242 (100%) similarity to human Newcastle disease virus inducible protein mRNA, partial 3' UTR region; 85/341 (24%) aa identity to human myosin heavy chain.
PSEC0251	2372	393	1	0.78	No & transmembrane	60/182 (32%) aa identity to EBV hypothetical BHLF1 protein
PSEC0256	3520		1		No & transmembrane	97/362 (26%) aa identity to rat cadherin-6 precursor; 1174/1394 (84%) similarity to mRNA for KIAA0345

(注) PSEC0067 & PSEC0239 : 5'-末端配列が、どちらもGenBankのdbESTの配列よりも長い。

(注 3) ATGpr1の値がやや低いクローン (PSEC0067, ATGpr1 0.26; PSEC0239, ATGpr1 0.18) : PSEC0067は、5'-端配列データ (one pass sequencing) をATGprで選別はしておらず、5'-端配列データからシグナル配列をもち、かつ、5'-端配列データでのORFの長いものとして選別してきたクローンを全長cDNA配列解析

したものである。PSEC0239は、5'-端配列データ (one pass sequencing) からAT Gpr1の値が高くシグナル配列を持つと予測して選別したクローンである。これらのクローンは、全長解析後に予測されるORFより、N-末端にシグナル配列が存在しないとの解析結果になったが、MEMSATとSOSUIで膜タンパク質 (transmembrane helixをもつ) であると予測された。また、以上2クローンについてESTとの比較をした結果、ESTに対してcDNAの5'-端側に長いクローンであると判定された。

(注4) PSEC0242とPSEC0251: 両クローンは3番目のATGから翻訳がはじまるとすると「N-末端にシグナル配列が存在」のカテゴリーに入る。

PSEC0242: No.3 ATG, ATGpr1 0.82, SP-Yes, ORF 171-1343 391 aa, Signal peptide 24;

PSEC0251: No.3 ATG, ATGpr1 0.77, SP-Yes, ORF 116-1256 380 aa, Signal peptide 28.

【0024】

更に本発明による168種のタンパク質のうち残る2種は、表10に示すcDNAクローン (PSEC0195、および PSEC0206)によってコードされている。SwissProtとの相同性より、PSEC0195はmouse plasma membrane adaptor HA2/AP2 adaptin alpha C subunitと、PSEC0206は分泌顆粒に存在するhuman carboxypeptidase H precursor (prohormone processing carboxypeptidase)に比較的高い相同性が見られた。したがって、これらのタンパク質は、分泌タンパク質あるいは膜タンパク質のカテゴリーに入る。

【0025】

【表10】

クローン 番号	cDNAサイズ (bp)	アミノ酸	ATG No.	ATGpr1	SP & MEMSAT	アノテーション
PSEC0195	1979	467	2	0.80	No	278/281 (98%) aa identity to mouse alpha-adaptin (C)
PSEC0206	1606	430	3	0.90	No	196/397 (49%) aa identity to human carboxypeptidase H

【0026】

本発明の分泌タンパク質、あるいは膜タンパク質は、そのアミノ酸配列が明らかとなっていることから、適当な発現系を適用して組み換え体として発現させることにより、あるいは、そのタンパクを特異的に認識する抗体を用いることで、

その生物学的活性を解析することが可能である。

分泌タンパク質、あるいは膜タンパク質は、例えば「The Practical Approach Series」(IRL PRESS社)の『Glycobiology』(M.Fukuda, A.Kobata編、1993)、『Growth Factors』(I.McKay, I.Leigh編、1993)、『Extracellular Matrix』(M.A.Haralson, J.R.Hassell編、1995)、または、「Method in Molecular Biology」(Humana Press社)シリーズの『Glycoprotein Analysis in Biomedicine』(Elizabeth F.Hounsell編、1993)にもとづいて、それぞれのタンパク質の生物学的活性の解析が可能である。あるいは「日本生化学会編 新生化学実験講座7 増殖分化因子とその受容体」(1991年発行)東京化学同人社や「Methods in Enzymology」Academic Press社のVolume 296 Neurotransmitter Transporters, Volume 294 Ion Channels (Part C), Volume 293 Ion Channels (Part B), Volume 292 ABC Transporters, Volume 288 Chemokine Receptors, Volume 287 Chemokines, Volume 248 Proteolytic Enzymes, Volume 245 Extracellular Matrix Components, Volume 244 Proteolytic Enzymes, Volume 230 Guide to Techniques in Glycobiology, Volume 198 Peptide Growth Factors, Volume 192 Biomembranes, Volume 191 Biomembranes, Volume 149 Drug and Enzyme Targeting等の開示に基づいて、分泌タンパク質や膜タンパク質に関連する生物学的活性を解析することもできる。

分泌タンパク質や膜タンパク質について、Online Mendelian Inheritance in Man (OMIM)(<http://www.ncbi.nlm.nih.gov/0mim/>)を利用し、下記検索キーワードを用いて検索すると、各キーワードにおいて、多くの疾患に関連した以下に示す結果が得られた。あるいは、例えば、このように、分泌タンパク質や膜タンパク質は疾患に関与することが多く、医療産業上の標的分子として、有用なことが分かる。

OMIM検索に用いたキーワード

- (1) secretion protein (分泌タンパク質)
- (2) membrane protein, (膜タンパク質)

検索結果には、OMIM登録番号のみを記載した。この番号をもとにOMIMで疾患と遺伝子やタンパク質との関係を示すデータを見ることができる。また、OMIMデー

タは日々更新されている。

【0027】

1) Secretion protein (分泌タンパク質)

268 entries found, searching for "secretion protein"

104760, 176860, 160900, 107400, 118910, 139320, 603850, 147572, 176880,
600946, 603215, 157147, 600174, 151675, 170280, 179512, 179513, 138120,
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179490, 185860, 603216, 122559, 601746, 147290, 602672, 146770, 603062,
179508, 131230, 601591, 602421, 139250, 167805, 167770, 600041, 600564,
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182100, 264300, 603795, 184600

【 0 0 2 8 】

2) Membrane protein (膜タンパク質)

1017 entries found, searching for "membrane protein"

130500, 305360, 153330, 173610, 170995, 109270, 170993, 309060, 120920,
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【 0 0 3 1 】

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【 0 0 3 6 】

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171833, 102573, 101800, 603875, 601108

【 0 0 3 7 】

分泌タンパク質、あるいは膜タンパク質を用いた機能の解析に基づいて、例えば以下のようにして医薬品開発を行うことができる。

膜タンパク質の場合、細胞上に発現して受容体やリガンドとして機能するタンパク質である可能性が高い。したがって、本発明によって提供される膜タンパク質を、公知のリガンドや受容体との結合活性に基づいてスクリーニングすれば、新たなリガンド-受容体の関係を見出すことができる。スクリーニングは公知の方法に従って行うことができる。

例えば、以下のようにして本発明のタンパク質の受容体を発現する細胞をスクリーニングすることができる。すなわち、(a) 本発明のタンパク質またはその部分ペプチドに被検細胞試料を接触させる工程、および (b) 該タンパク質またはその部分ペプチドに結合する細胞を選択する工程、とによって特定のタンパク質に結合する受容体のスクリーニングが可能である。

【 0 0 3 8 】

このスクリーニングは、例えば、以下のように行うことが可能である。まず、本発明のタンパク質を発現させ組換えタンパク質の精製品を取得する。次いで、その精製タンパク質を標識し、各種細胞株または初代培養細胞に対して結合アッセイを行い、これにより受容体を発現している細胞を選定する（本庶・新井・谷口・村松編 新生化学実験講座 7 増殖分化因子とその受容体 p203-236 (1991) 東京化学同人）。標識としては、¹²⁵I などの RI 標識のほか、酵素（アルカリホスファターゼ等）標識も可能である。また、本発明のタンパク質を標識せずに用いて、本発明のタンパク質に対する抗体を標識して用いて検出することも考えられる

。上記スクリーニングにより得られた本発明のタンパク質の受容体を発現する細胞は、後述するように該受容体のアゴニストやアンタゴニストのスクリーニングに用いることが可能である。

上記のスクリーニングにより本発明のタンパク質の受容体やその受容体を発現する細胞が得られれば、本発明のタンパク質とその受容体または該受容体を発現する細胞との結合活性を指標に、両者の結合を阻害する化合物（例えば、受容体アゴニストやアンタゴニスト）のスクリーニングが可能となる。

【0039】

このスクリーニング方法は、（a）被検試料の存在下で、本発明のタンパク質を該タンパク質の受容体または該受容体を発現する細胞に接触させる工程、（b）該タンパク質とその受容体または該受容体を発現する細胞との結合活性を検出する工程、および（c）被検試料非存在下において検出した場合と比較して、該結合活性を低下させる化合物を選択する工程、を含む。

スクリーニングに用いる被検試料としては、例えば、細胞抽出液、遺伝子ライブラリーの発現産物、合成低分子化合物、合成ペプチド、天然化合物などが挙げられるが、これらに制限されない。また、本発明のタンパク質との結合活性を指標とした上記のスクリーニングにより単離された化合物を被検試料として用いることも可能である。

このスクリーニングにより単離される化合物は、本発明のタンパク質の受容体のアゴニストやアンタゴニストの候補となる。本発明のタンパク質とその受容体との結合活性の低下によるリン酸化などの細胞内シグナルの変化をもとに、得られた化合物が本発明のタンパク質の受容体のアゴニストであるかアンタゴニストであるかを判定することができる。また、得られる化合物は、生体内において、本発明のタンパク質と相互作用する分子（受容体も含む）との該相互作用を阻害する化合物の候補ともなる。これら化合物は、本発明のタンパク質が関連する疾患の予防薬や治療薬への応用が考えられる。

【0040】

分泌タンパク質の場合、細胞の増殖・分化などの細胞状態を制御する因子の可能性がある。新たな細胞状態を制御する因子を見いだすためには、ある種の細胞

に、本発明によって提供される分泌タンパク質を加えることによって、細胞の増殖・分化などの細胞状態変化や、細胞内の特定の遺伝子の活性化を指標にスクリーニングすれば可能である。

このスクリーニングは、例えば、以下のように行うことが可能である。まず、本発明のタンパク質を発現させ組換えタンパク質の精製品を取得する。次いで、その精製タンパク質を、各種細胞株または初代培養細胞に添加して、増殖・分化などの細胞の変化を調べる。または、ある特定の細胞状態変化に作用することが知られている遺伝子の誘導をmRNA量、タンパク質量で検出する。あるいはある特定の細胞状態変化に作用することが知られている遺伝子産物（タンパク質）の働きにより変化した細胞内の物質（低分子化合物など）量で検出する。

このようなスクリーニングにより、本発明によるタンパク質が細胞状態、機能を制御するとなれば、本発明のタンパク質は、関連した疾患に対して、そのまま、あるいは一部適した状態に改変して、医薬品への応用が考えられる。

また、先に膜タンパクについて記述したように、本発明によって提供される分泌タンパク質を用いて、公知のリガンドや受容体との結合活性に基づいてスクリーニングすれば、新たなリガンド-受容体の関係を見出すことができ、同様の方法でアゴニスト、アンタゴニストの判定が可能となる。こうして得られる化合物は、生体内において、本発明のタンパク質と相互作用する分子(受容体も含む)との該相互作用を阻害する化合物の候補ともなる。これら化合物は、本発明のタンパク質が関連する疾患の予防薬や治療薬への応用が考えられる。

【0-0-4-1】

あるいは、このようなスクリーニングにより影響を受けたタンパク質や遺伝子が疾患に関連していた場合、本発明によるタンパク質を利用し、直接的に、または、間接的に、その発現や活性調節を行う化合物、遺伝子のスクリーニングが可能となる。

例えば、まず、本発明のタンパク質を発現させ組換えタンパク質の精製品を取得する。次に影響を受けたタンパク質や遺伝子を精製し、その結合に基づいてスクリーニングを行う。または、予め阻害剤の候補となる化合物を加えておいた後、それら結合の変化を観察することによってスクリーニングを行う。このような

スクリーニングによって得られた化合物は、本発明によるタンパク質が関連した疾患に対して医薬品への応用が考えられる。スクリーニングによって得られた制御因子がタンパク質であっても、同様に、そのタンパク質の発現・活性に本来ない影響を与える化合物があれば、その化合物は、本発明によるタンパク質が関連した疾患に対して医薬品への応用が考えられる。

【0042】

本発明による分泌タンパク質、あるいは膜タンパク質が酵素としての活性を有するとなれば、本発明によって提供されるタンパク質に化合物を適当な条件下で添加し、化合物の変化を指標としてその活性を明らかにすることができる。また、この活性を指標に本発明によるタンパク質の活性を阻害する化合物のスクリーニングも可能である。

このスクリーニングは、例えば、以下のように行うことが可能である。まず、本発明のタンパク質を発現させ組換えタンパク質の精製品を取得する。次いで、その精製タンパク質に、化合物を添加して、化合物量および反応生成物量を調べる。または、予め阻害剤の候補となる化合物を加えておいた後、精製タンパク質と反応する化合物（基質）を加えて、その基質量および反応生成物量の変化を調べる。

このようなスクリーニングにより、得られた化合物は、本発明のタンパク質が関連した疾患に対して、医薬品への応用が考えられる。

本発明の分泌タンパク質、あるいは膜タンパク質が、新たな疾患関連タンパク質であるかどうかは、上記に挙げた以外にも、本発明によるタンパク質の特異認識抗体を用いて、特定の疾患とタンパク質の発現量や活性との相関を調べることでより知ることができる。あるいは、「Method in Molecular Biology」(Humana Press社)シリーズの『Molecular Diagnosis of Genetic Diseases』(Rob Elless編、1996)を参考に解析が可能である。

【0043】

本発明の分泌タンパク質、または膜タンパク質は、組み換えタンパク質として、また天然のタンパク質として調製することが可能である。組み換えタンパク質は、例えば、後述するように本発明のタンパク質をコードするDNAを挿入したベ

クターを適当な宿主細胞に導入し、形質転換体内で発現したタンパク質を精製することにより調製することが可能である。一方、天然のタンパク質は、例えば、後述する本発明のタンパク質に対する抗体を結合したアフィニティーカラムを利用して調製することができる (Current Protocols in Molecular Biology edit. Ausubel et al. (1987) Publish. Jhon Wily & Sons Section 16.1-16.19)。アフィニティー精製に用いる抗体は、ポリクローナル抗体であってもモノクローナル抗体であってもよい。また、インビトロトランスレーション (例えば、「On the fidelity of mRNA translation in the nuclease-treated rabbit reticulocyte lysate system. Dasso, M.C., Jackson, R.J. (1989) NAR 17:3129-3144」参照) などにより本発明のタンパク質を調製することも可能である。

【 0 0 4 4 】

本発明は、また、本発明のタンパク質の部分ペプチドを含む。この部分ペプチドには、例えば、分泌タンパク質におけるシグナルペプチドが除去されたタンパク質が含まれる。また、本発明のタンパク質が受容体やリガンドとしての活性を持つものの場合には、その競合阻害剤として機能する、受容体 (あるいはリガンド) との結合能を有する部分ペプチドが含まれる。また、抗体調製のための抗原ペプチドが含まれる。部分ペプチドが本発明のタンパク質に特異的であるためには、少なくとも7アミノ酸、好ましくは8アミノ酸以上、より好ましくは9アミノ酸以上のアミノ酸配列からなる。該部分ペプチドは、本発明のタンパク質に対する抗体や本発明のタンパク質の競合阻害剤の調製以外に、例えば、本発明のタンパク質に結合する受容体のスクリーニングなどに利用し得る。本発明の部分ペプチドは、例えば、遺伝子工学的手法、公知のペプチド合成法、あるいは本発明のタンパク質を適当なペプチダーゼで切断することによって製造する。

【 0 0 4 5 】

また、本発明は、上記本発明のタンパク質をコードするDNAに関する。本発明のDNAとしては、本発明のタンパク質をコードしうるものであれば、その形態に特に制限はなく、cDNAの他、ゲノムDNA、化学合成DNAなども含まれる。また、本発明のタンパク質をコードしうる限り、遺伝暗号の縮重に基づく任意の塩基配列を有するDNAが含まれる。本発明のDNAは、上記のように、配列番号：1～配列番

号：335の奇数番号に示す塩基配列もしくはその一部をプローブとしたハイブリダイゼーション法やこれらDNA配列をもとに合成したプライマーを用いたPCR法等の常法により単離することが可能である。

たとえば実施例において単離した本発明によるすべてのクローン（168クローン）は新規で、全長であり、かつ膜タンパク質、あるいは分泌タンパク質をコードするものである。本発明に基づくすべてのcDNAクローンは、次のように特徴付けることもできる。

【0046】

すなわち、オリゴキャップ法で取得された全長性の高いcDNAであり、その5'末端配列データの特徴をもとに、5'末端の全長性を予測するATGpr（あるいはATGpr1と記載している）のスコアにより選別されており、さらにシグナル配列の存在を予測するPSORTにより5'末端にシグナル配列、あるいはタンパクコーディング領域中に膜貫通領域を有するものが選別されている。また、選別されたクローンは5'末端配列の相同性検索によりヒトmRNAに対して同一でない（すなわち新規である）ことがわかっている。

【0047】

また、本発明は、本発明のDNAが挿入されたベクターに関する。本発明のベクターとしては、挿入したDNAを安定に保持するものであれば特に制限されず、例えば宿主に大腸菌を用いるのであれば、クローニング用ベクターとしてはpBlue scriptベクター（Stratagene社製）などが好ましい。本発明のタンパク質を生産する目的においてベクターを用いる場合には、特に発現ベクターが有用である。

発現ベクターとしては、試験管内、大腸菌内、培養細胞内、生物個体内でタンパク質を発現するベクターであれば特に制限されないが、例えば、試験管内発現であればpBESTベクター（プロメガ社製）、大腸菌であればpETベクター（Invitrogen社製）、培養細胞であればpME18S-FL3ベクター（GenBank Accession No. AB009864）、生物個体であればpME18Sベクター（Mol Cell Biol. 8:466~472(1988)）などが好ましい。ベクターへの本発明のDNAの挿入は常法により制限酵素サイトをういたりガーゼ反応により行うことができる（Current protocols in Molecular Biology edit. Ausubel et al. (1987) Publish. John Wiley & Sons. Se

ction 11.4～11.11)。

【0048】

また、本発明は、本発明のベクターを保持する形質転換体に関する。本発明のベクターが導入される宿主細胞としては特に制限はなく、目的に応じて種々の宿主細胞が用いられる。タンパク質を高発現させるための真核細胞としては、例えば、COS細胞、CHO細胞などを例示することができる。

【0049】

宿主細胞へのベクター導入は、例えば、リン酸カルシウム沈殿法、電気パルス穿孔法 (Current protocols in Molecular Biology edit. Ausubel et al. (1987) Publish. John Wiley & Sons. Section 9.1-9.9)、リポフェクタミン法 (GIBCO-BRL社製)、マイクロインジェクション法などの方法で行うことが可能である。

【0050】

また本発明は、本発明のタンパク質をコードする配列番号：1～配列番号：335の奇数番号に記載の塩基配列からなるDNA、またはその相補鎖と特異的にハイブリダイズし、少なくとも15ヌクレオチドの鎖長を有するDNAに関する。ここで「特異的にハイブリダイズする」とは、通常のハイブリダイゼーション条件下、好ましくは厳格な条件下で、本発明のタンパク質をコードする配列番号：1～配列番号：335の奇数番号に記載のDNA、またはその相補鎖とハイブリダイズし、他のタンパク質をコードするDNAとはハイブリダイズしないことを意味する。

このようなDNAは、本発明のDNAを検出、単離するためのプローブとして、また

、本発明のDNAを増幅するためのプライマーとして利用することが可能である。プライマーとして用いる場合には、通常、15bp～100bp、好ましくは15bp～35bpの鎖長を有する。また、プローブとして用いる場合には、本発明のDNAの少なくとも一部若しくは全部の配列を有し、少なくとも15bpの鎖長のDNAが用いられる。

【0051】

本発明のDNAは、本発明のタンパク質の異常を検査・診断するために利用できる。例えば、本発明のDNAをプローブやプライマーとして用いたノーザンハイブ

リダイゼーションやRT-PCRにより、発現異常を検査したり、本発明のDNAをプライマーとして用いたポリメラーゼ連鎖反応(PCR)によりゲノムDNA-PCRやRT-PCRにより本発明のタンパク質をコードするDNAやその発現制御領域を増幅し、RFLP解析、SSCP、シーケンシング等の方法により、配列の異常を検査・診断することができる。

【0052】

また、「配列番号：1～配列番号：335の奇数番号に記載の塩基配列からなるDNA、またはその相補鎖と特異的にハイブリダイズし、少なくとも15ヌクレオチドの鎖長を有するDNA」には、本発明のタンパク質の発現を抑制するためのアンチセンスDNAが含まれる。アンチセンスDNAは、アンチセンス効果を引き起こすために、少なくとも15bp以上、好ましくは100bp、さらに好ましくは500bp以上の鎖長を有し、通常、3000bp以内、好ましくは2000bp以内の鎖長を有する。このようなアンチセンスDNAには、本発明のタンパク質の異常（機能異常や発現異常）などに起因した疾患の遺伝子治療への応用も考えられる。該アンチセンスDNAは、例えば、本発明のタンパク質をコードするDNA（例えば、配列番号：1～配列番号：335の奇数番号に記載のDNA）の配列情報を基にホスホロチオネート法（Stein, 1988 Physicochemical properties of phosphorothioate oligodeoxynucleotides. Nucleic Acids Res 16, 3209-21 (1988)）などにより調製することが可能である。

【0053】

本発明のDNAまたはアンチセンスDNAは、遺伝子治療に用いる場合には、例えば、レトロウイルスベクター、アデノウイルスベクター、アデノ随伴ウイルスベクターなどのウイルスベクターやリポソームなどの非ウイルスベクターなどを利用して、ex vivo法やin vivo法などにより患者へ投与を行う。

【0054】

また、本発明は、本発明のタンパク質に結合する抗体に関する。本発明の抗体の形態には特に制限はなく、ポリクローナル抗体やモノクローナル抗体または抗原結合性を有するそれらの一部も含まれる。また、全てのクラスの抗体が含まれる。さらに、本発明の抗体には、ヒト化抗体などの特殊抗体も含まれる。

【0055】

本発明の抗体は、ポリクローナル抗体の場合には、常法に従いアミノ酸配列に相当するオリゴペプチドを合成して家兎に免疫することにより得ることが可能であり (Current protocols in Molecular Biology edit. Ausubel et al. (1987) Publish. John Wiley & Sons. Section 11.12~11.13)、一方、モノクローナル抗体の場合には、常法に従い大腸菌で発現し精製したタンパク質を用いてマウスを免疫し、脾臓細胞と骨髓腫細胞を細胞融合させたハイブリドーマ細胞の中から得ることができる (Current protocols in Molecular Biology edit. Ausubel et al. (1987) Publish. John Wiley & Sons. Section 11.4~11.11)。

【0056】

本発明のタンパク質に結合する抗体は、本発明のタンパク質の精製に加え、例えば、本発明のタンパク質の発現異常や構造異常の検査・診断に利用することも考えられる。具体的には、例えば組織、血液、または細胞などからタンパク質を抽出し、ウェスタンブロッティング、免疫沈降、ELISA等の方法による本発明のタンパク質の検出を通して、発現や構造の異常の有無を検査・診断することができる。

【0057】

また、本発明のタンパク質に結合する抗体を、本発明のタンパク質に関連した疾患の治療などの目的に利用することも考えられる。抗体を患者の治療目的で用いる場合には、ヒト抗体またはヒト化抗体が免疫原性の少ない点で好ましい。ヒト抗体は、免疫系をヒトのものと入れ換えたマウス (例えば、「Functional tra

nsplant of megabase human immunoglobulin loci recapitulates human antibody response in mice, Mendez, M.J. et al. (1997) Nat. Genet. 15:146-156」参照) に免疫することにより調製することができる。また、ヒト化抗体は、モノクローナル抗体の超可変領域を用いた遺伝子組み換えによって調製することができる (Methods in Enzymology 203, 99-121 (1991))。

【0058】

【実施例】

次に、本発明を実施例によりさらに具体的に説明するが、本発明は下記実施例

に限定されるものではない。

実施例 1. オリゴキャップ法による cDNA ライブラリーの作製

ヒト胎児精巣由来のテラトカルシノーマ細胞でレチノイン酸処理により神経細胞に分化可能な NT-2 神経前駆細胞 (Stratagene 社より購入) を用いた。添付マニュアルに従って、次の条件で培養細胞を調製した。

- (1) NT-2 細胞をレチノイン酸で誘導しないで培養 (NT2RM1)
- (2) NT-2 細胞を培養後、レチノイン酸を添加して誘導後、48 時間培養 (NT2RP1)
- (3) NT-2 細胞を培養後、レチノイン酸を添加して誘導後、2 週間培養 (NT2RP2 と NT2RP3)

これらの培養細胞をそれぞれ集めて、文献 (J. Sambrook, E. F. Fritsch & T. Maniatis, Molecular Cloning Second edition, Cold Spring harbor Laboratory Press 1989) 記載の方法により mRNA を抽出した。さらに、オリゴdT セルロースで poly(A)⁺ RNA を精製した。

同様に、ヒト胎盤組織 (PLACE1)、ヒト卵巣癌組織 (OVARC1)、ヒト胎児より脳を多く含む組織 (HEMBA1) より、文献 (J. Sambrook, E. F. Fritsch & T. Maniatis, Molecular Cloning Second edition, Cold Spring harbor Laboratory Press, 1989) 記載の方法により mRNA を抽出した。さらに、オリゴdT セルロースで poly(A)⁺ RNA を精製した。

【 0 0 5 9 】

それぞれの poly(A)⁺ RNA よりオリゴキャップ法 [M. Maruyama and S. Sugano, Gene, 138: 171-174 (1994)] により cDNA ライブラリーを作成した。Oligo-cap linker (配列番号: 3 3 7) およびオリゴdT プライマー (配列番号: 3 3 8) を用いて文献 [鈴木・菅野, 蛋白質 核酸 酵素, 41: 197-201 (1996)、Y. Suzuki et al., Gene, 200: 149-156 (1997)] の記載にしたがって BAP (Bacterial Alkaline Phosphatase) 処理、TAP (Tobacco Acid Phosphatase) 処理、RNA ライゲーション、第一鎖 cDNA の合成と RNA の除去を行った。次いで、5' (配列番号: 3 3 9) と 3' (配列番号: 3 4 0) の PCR プライマーを用い PCR (polymerase chain reaction) により 2 本鎖 cDNA に変換し、SfiI 切断した。次いで、DraIII で切断したべ

クターpUC19FL3 (図1) (NT2RM1とNT2RP1) またはpME18SFL3 (図1) (GenBank AB009864, Expression vector) (NT2RP2, NT2RP3, PLACE1, OVARC1, HEMBA1) にcDNAの方向性を決めてクローニングし、cDNAライブラリーを作成した。これらより得たクローンのプラスミドDNAについて、NT2RM1, NT2RP1, NT2RP2, PLACE1, OVARC1, HEMBA1については、挿入cDNAサイズが1 kb以下のクローンを、また、NT2RP3については、挿入cDNAサイズが2 kb以下のクローンを除いた後、cDNAの5' 端と3' 端の塩基配列をDNAシーケンシング試薬 (Dye Terminator Cycle Sequencing FS Ready Reaction Kit, dRhodamine Terminator Cycle Sequencing FS Ready Reaction KitまたはBigDye Terminator Cycle Sequencing FS Ready Reaction Kit, PE Biosystems社製) を用い、マニュアルに従ってシーケンシング反応後、DNAシーケンサー (ABI PRISM 377, PE Biosystems社製) でDNA塩基配列を解析した。

【0060】

NT2RM1とNT2RP1以外のオリゴキャップ高全長率cDNAライブラリーは、真核細胞での発現が可能な発現ベクターpME18SFL3を用いて作製した。pME18SFL3にはクローニング部位の上流にSR α プロモーターとSV40 small tイントロンが組み込まれており、またその下流にはSV40ポリA付加シグナル配列部位が挿入されている。pME18SFL3のクローン化部位は非対称性のDraIIIサイトとなっており、cDNA断片の末端にはこれと相補的なSfiI部位を付加しているので、クローン化したcDNA断片はSR α プロモーターの下流に一方向性に挿入される。したがって、全長cDNAを含むクローンでは、得られたプラスミドをそのままCOS細胞に導入することにより、一過的に遺伝子を発現させることが可能である。すなわち、非常に容易に、遺伝子産物である蛋白質として、あるいはそれらの生物学的活性として実験的に解析することが可能となっている。

【0061】

オリゴキャップ法で作製したライブラリーのcDNAの5'-末端の全長率を次の方法で、求めた。公共データベース中のヒト既知mRNAと5'-末端配列が一致する全クローンについて、公共データベース中の既知mRNA配列より長く5'-末端が伸びている場合と5'-末端は短いが翻訳開始コドンは有している場合を「全長」と判

断し、翻訳開始コドンを含んでいない場合を「非全長」と判断した。各ライブラリーでのcDNAクローンの5'-末端の全長率〔全長クローン数／（全長クローン数＋非全長クローン数）〕をヒト既知mRNAと比較することにより求めた（NT2RM1：69%；NT2RP1：75%；NT2RP2：62%；NT2RP3：61%；PLACE1：68%；OVARC1：59%；HEMBA1：53%）。この結果より、5'-端配列の全長率が非常に高いことが分かった。

cDNAライブラリーとクローンとの関係は次のとおりである。

NT2RM1：PSEC0001-PSEC0017

NT2RP1：PSEC0019-PSEC0045

NT2RP2：PSEC0048-PSEC0085、PSEC0092-PSEC0109、

PSEC0111-PSEC0113、PSEC0173

NT2RP3：PSEC0241-PSEC0263

PLACE1：PSEC0086-PSEC0090、PSEC0110、

PSEC0117-PSEC0172

OVARC1：PSEC0178-PSEC0183、PSEC0239-PSEC0240

HEMBA1：PSEC0190-PSEC0236

【 0 0 6 2 】

実施例 2. ATGprとESTiMateFLでのcDNAの5'-末端の全長率の評価

ATGpr は、ATGコドンの周辺の配列の特徴から翻訳開始コドンであるかどうかを予測するためにヘリックス研究所のA. A. Salamov, T. Nishikawa, M. B. Swindellsにより開発したプログラムである。結果は、そのATGが真の開始コドンである期待値で表した（0.05-0.94）。尚、このプログラムのcDNAの5'-末端である

かどうかを考慮しない場合の解析結果の感度と特異性はともに66%と評価している。一方、このプログラムを全長率65%のオリゴキャップ法で作製したライブラリーからのcDNAクローンの5'-末端配列に適用してATGpr1値を0.6以上でクローンを選択した場合、全長クローン（ORFのN-末端までもつクローン）評価の感度と特異性はともに82～83%まで上昇した。さらに、このプログラムをオリゴキャップ法で作製したヒトcDNAライブラリーからのクローンの5'-末端配列が既知ヒトmRNAと一致する17,365クローンについて評価した結果を示す。すなわち、既知ヒトmRNAと一致するクローンについてATGpr1の最大値を求め、次いで各クローンの

5'-末端配列を既知ヒト mRNA の ORF と比較し、全長か非全長かを決定した。その結果をまとめたものを表 11 に示した。ATGpr とオリゴキャップ法で作製したヒト cDNA ライブラリーからのクローンの組み合わせによる選択が、非常に有効なことを示している。

【0063】

【表 11】

ATGpr1 の 最大値	(全長+非全長) の数	全長の数	全長率
>=0.70	10,226	8,428	82.4%
>=0.50	12,171	9,422	77.4%
>=0.30	14,102	10,054	71.3%
>=0.17	15,647	10,385	66.4%
>=0.05	17,365	10,608	61.1%

* 全長の数：ORF の N-末端までもつクローンの数；非全長の数：ORF の N-末端まで持っていないクローンの数；全長率：全長の数 / (全長+非全長) の数

【0064】

ESTiMateFL は、公共データベース中の EST の 5'-末端配列や 3'-末端配列との比較による全長 cDNA の可能性の高いクローンを選択するヘリックス研究所の西川・

太田らにより開発された方法である。

この方法は、ある cDNA クローンの 5'-末端や 3'-末端配列よりも、長く伸びた EST が存在する場合には、そのクローンは「全長ではない可能性が高い」と判断する方法で、大量処理可能なようにシステム化したものである。公共データベース中の EST 配列より長く 5'-末端が伸びている場合、および 5'-末端が短いクローンでも両者の差が 50 塩基以内である場合を便宜的に全長とし、それ以上短い場合を非全長とした。EST との比較による完全長らしさの評価では、比較対照とする EST の数が多ければ予測精度は高まるが、対象 EST が少ない場合には予測結果の信頼

性が低くなる欠点はある。この方法は、5'-末端配列での全長率が約60%のオリゴキャップ法によるcDNAクローンから全長ではない可能性の高いクローンを排除するのに使えば有効である。また、ESTiMateFLは、公共データベースへのEST登録が適当数あるヒト未知mRNAのcDNAの3'-末端配列の全長性を評価するには、特に有効な方法である。

【0065】

その結果をまとめたものを表12、および表13に示した。ATGprとESTiMateFLの両プログラムを組み合わせて、オリゴキャップ法で作製したヒトcDNAライブラリーからのクローンの5'-末端配列の全長性を評価すれば、ATGprの値の低いクローンでも全長率が高くなることが確認された。この結果を全長cDNA配列を決めたクローンの5'-末端配列の全長性の評価に応用した。なお表中、全長の数とはORFのN-末端までもつクローンの数、非全長の数とはORFのN-末端までもっていないクローンの数、そして全長率とは全長の数/(全長+非全長)の数を意味する。

【0066】

【表12】

既知ヒトmRNAのORFと比較し、全長であると判定したオリゴキャップ法で取得したcDNAクローンの5'-末端配列のESTに対する全長率

ATGpr1の 最大値	(全長+非全長) の数	非全長 の数	全長率
>=0.30	8,646	907	90.5%
>=0.17	10,158	1,150	89.8%
>=0.05	15,351	2,728	84.9%

【0067】

【表13】

既知ヒトmRNAのORFと比較し、非全長であると判定したオリゴキャップ法で取得

したcDNAクローンの5'-末端配列のESTに対する全長率

ATGpr1の 最大値	(全長+非全長) の数	非全長 の数	全長率
>=0.30	1,271	2,156	37.1%
>=0.17	1,678	2,907	36.6%
>=0.05	2,512	4,529	35.7%

【0068】

実施例3. シグナル配列をもつクローンの選択とそれより全長率の高いクローンの選択

オリゴキャップ法で作成した各ライブラリーのクローンから、5'-末端配列の中のすべてのATGコドンから予測される推定アミノ酸配列について、中井・金久が開発したタンパク質の局在性予測プログラム「PSORT」を用い、多くの分泌タンパク質のアミノ末端に特徴的なシグナルペプチドと予測される配列の有無を解析することにより、シグナル配列をもつと予測されるクローン（分泌タンパク質、または膜タンパク質の可能性が高い）を特異的に選別した。

PSEC0001-PSEC0067については、5'-端配列データ（one pass sequencing）に基づくATGprによる選別はしていない。しかし5'-端配列データからシグナル配列（PSORTで解析）を持ち、かつ、5'-端配列データでのORF（アミノ酸翻訳領域）

が存在するものを選別したクローンである。また、PSEC0068-PSEC0263については、5'-端配列データ（one pass sequencing）からATGpr1の最大値が0.7以上で、シグナル配列（PSORTで解析）を持ち、かつ、5'-端配列データでのORFが存在するものを選別したクローンである。

【0069】

実施例4. 全長cDNA配列解析とカテゴリー分別

実施例3で選択した172クローンについて、全長cDNAの塩基配列、並びに推定アミノ酸配列を決定した。塩基配列は、次に示す3種の方法を組み合わせ、各

方法によって決定した塩基配列を完全にオーバーラップさせ、最終的な確定塩基配列を決定した。決定されたcDNA配列から、推定アミノ酸配列を明らかにした。それらの結果を配列表に示した。(分泌タンパク質、または膜タンパク質に分別した168クローンについてのみ)

(1) Licor DNAシーケンサーを用いたcDNA挿入断片両末端からのロングリードシーケンス(Licorシーケンサー(アロカ社販売)のマニュアルに従ってシーケンシング反応後、LicorシーケンサーでDNA塩基配列を解析した)、

(2) AT2トランスポゾン試験管内転移を用いたPrimer Island法によるネステッドシーケンス[S. E. Devine and J. D. Boeke, Nucleic Acids Res., 22: 3765-3772, (1994)](PE Biosystems社製のキットとマニュアルにしたがってクローンを取得後、PE Biosystems社製のDNAシーケンシング試薬でマニュアルに従ってシーケンシング反応し、ABI PRISM 377でDNA塩基配列を解析した)

(3) カスタム合成DNAプライマーを用いたダイデオキシターミネーター法によるプライマーウォーキング(カスタム合成DNAプライマーをもちいPE Biosystems社製のDNAシーケンシング試薬でマニュアルに従ってシーケンシング反応し、ABI PRISM 377でDNA塩基配列を解析した)

【0070】

これらの配列について、ATGprとPSORTによる解析およびGenBankやSwissProtに対するBLAST解析を行った。ほとんどのクローン(172クローン中152クローン)がN-末端にシグナル配列をもつ分泌タンパク質、または膜タンパク質であると推定された。さらに、PSORTでシグナル配列が検出されなかったクローン(P

SEC0027, PSEC0047, PSEC0066, PSEC0067, PSEC0069, PSEC0092, PSEC0103, PSEC0117, PSEC0142, PSEC0212, PSEC0239, PSEC0242, PSEC0251, PSEC0256, PSEC0006, PSEC0043, PSEC0058, PSEC0195, PSEC0206, PSEC0211)については、MEMSATおよびSOSUIで膜タンパク質(transmembrane helixをもつ)と予測できるかどうかを検索した。その結果、20クローン中の14クローン(PSEC0027, PSEC0047, PSEC0066, PSEC0067, PSEC0069, PSEC0092, PSEC0103, PSEC0117, PSEC0142, PSEC0212, PSEC0239, PSEC0242, PSEC0251, PSEC0256)にtransmembrane helixが存在すると予測された。これらは、膜タンパク質であると推定された。また

、SwissProtとの相同性より、PSEC0195はmouse plasma membrane adaptor HA2/A P2 adaptin alpha C subunitと、PSEC0206は分泌顆粒に存在するhuman carboxypeptidase H precursor (prohormone processing carboxypeptidase)に比較的高い相同性が見られた。

【0071】

以上の結果を表2～表10に示した。各cDNAクローンの機能annotationも同じ表中に示した。また、168クローンのカテゴリーを次に示す。

1. 分泌タンパク質、または膜タンパク質で全長cDNAクローンであると予測されるクローン (168クローン)

(ほとんどのクローンのATGpr1の値が0.5以上)

1) 分泌タンパク質、または膜タンパク質でN-末端にシグナル配列が存在し、全長cDNAクローンであると予測されるクローン (152クローン、表2～表8)

PSEC0001 PSEC0049 PSEC0085 PSEC0113

PSEC0004 PSEC0051 PSEC0086 PSEC0119

PSEC0005 PSEC0052 PSEC0087 PSEC0120

PSEC0007 PSEC0053 PSEC0088 PSEC0121

PSEC0008 PSEC0055 PSEC0090 PSEC0124

PSEC0012 PSEC0059 PSEC0094 PSEC0125

PSEC0017 PSEC0061 PSEC0095 PSEC0126

PSEC0019 PSEC0068 PSEC0098 PSEC0127

PSEC0020 PSEC0070 PSEC0099 PSEC0128

PSEC0021 PSEC0071 PSEC0100 PSEC0129

PSEC0028 PSEC0072 PSEC0101 PSEC0130

PSEC0029 PSEC0073 PSEC0104 PSEC0131

PSEC0030 PSEC0074 PSEC0105 PSEC0133

PSEC0031 PSEC0075 PSEC0106 PSEC0134

PSEC0035 PSEC0076 PSEC0107 PSEC0135

PSEC0038 PSEC0077 PSEC0108 PSEC0136

PSEC0040 PSEC0079 PSEC0109 PSEC0137

PSEC0041 PSEC0080 PSEC0110 PSEC0139
PSEC0045 PSEC0081 PSEC0111 PSEC0143
PSEC0048 PSEC0082 PSEC0112 PSEC0144

PSEC0146 PSEC0178 PSEC0216 PSEC0247
PSEC0147 PSEC0181 PSEC0218 PSEC0248
PSEC0149 PSEC0182 PSEC0220 PSEC0249
PSEC0150 PSEC0183 PSEC0222 PSEC0250
PSEC0151 PSEC0190 PSEC0223 PSEC0252
PSEC0152 PSEC0191 PSEC0224 PSEC0253
PSEC0158 PSEC0192 PSEC0226 PSEC0255
PSEC0159 PSEC0197 PSEC0227 PSEC0258
PSEC0161 PSEC0198 PSEC0228 PSEC0259
PSEC0162 PSEC0199 PSEC0230 PSEC0260
PSEC0163 PSEC0200 PSEC0232 PSEC0261
PSEC0164 PSEC0203 PSEC0233 PSEC0263
PSEC0165 PSEC0204 PSEC0235
PSEC0167 PSEC0205 PSEC0236
PSEC0168 PSEC0207 PSEC0240
PSEC0169 PSEC0209 PSEC0241
PSEC0170 PSEC0210 PSEC0243

PSEC0171 PSEC0213 PSEC0244
PSEC0172 PSEC0214 PSEC0245
PSEC0173 PSEC0215 PSEC0246

(注 1) ATGpr1の値が0.5以下のクローン (PSEC0017, ATGpr1 0.33; PSEC0030, ATGpr1 0.26; PSEC0031, ATGpr1 0.20; PSEC0049, ATGpr1 0.35) : これらのクローンは、5'-端配列データ (one pass sequencing) をATGprで選別はしておらず、5'-端配列データからシグナル配列をもち、かつ、5'-端配列データでのORFの長いものとして選別してきたクローンを全長cDNA配列解析したものである。

これらはすべてN-末端にシグナル配列が存在していた。また、以上4クローンのうちPSEC0049以外のものは、ESTとの比較の結果cDNAの5'末端側に長かった。またPSEC0049は、ESTと比較してcDNAのORFにおいて5'末端側に長かった。つまり、これらのクローンがいずれも全長cDNAであることが明らかである。

【0072】

2) 分泌タンパク質、または膜タンパク質でN-末端にシグナル配列は存在しないが膜タンパク質であり、全長cDNAクローンであると予測されるクローン (14クローン、表9)

PSEC0027

PSEC0047

PSEC0066

PSEC0067

PSEC0069

PSEC0092

PSEC0103

PSEC0117

PSEC0142

PSEC0212

PSEC0239

PSEC0242

PSEC0251

PSEC0256

(注3) ATGpr1の値が0.5以下のクローン (PSEC0067, ATGpr1 0.26; PSEC0239, ATGpr1 0.18) : PSEC0067は、5'-端配列データ (one pass sequencing) をATGprで選別はしておらず、5'-端配列データからシグナル配列をもち、かつ、5'-端配列データでのORFの長いものとして選別してきたクローンを全長cDNA配列解析したものである。PSEC0239は、5'-端配列データ (one pass sequencing) からATGpr1の値が高くシグナル配列を持つと予測して選別したクローンである。これらのクローンは、全長解析後に予測されるORFより、N-末端にシグナル配列が存在

しないとの解析結果になったが、MEMSATおよびSOSUIで膜タンパク質 (transmembrane helixをもつ) であると予測された。また、以上2クローンについてESTとの比較をした結果、ESTに対してcDNAの5'側に長いクローンであると判定された。

(注4) PSEC0242とPSEC0251: 両クローンは3番目のATGから翻訳がはじまるとすると"N-末端にシグナル配列が存在"のカテゴリーに入る。

PSEC0242: No.3 ATG, ATGpr1 0.82, SP-Yes, ORF 171-1343 391 aa, Signal peptide 24;

PSEC0251: No.3 ATG, ATGpr1 0.77, SP-Yes, ORF 116-1256 380 aa, Signal peptide 28.

【0073】

2. PSORT、MEMSAT、およびSOSUIの解析からは非分泌タンパク質、かつ非膜タンパク質だが、全長率の高いオリゴキャップ法で作成したヒトcDNAライブラリーから、ATGpr等で全長cDNAであると予測されるクローン (6クローン)

(ほとんどのクローンATGpr1の値が0.5以上)

PSEC0006、PSEC0043、PSEC0058、PSEC0195、PSEC0206、PSEC0211

SwissProtとの相同性より、PSEC0195はmouse plasma membrane adaptor HA2/A P2 adaptin alpha C subunitと、PSEC0206は分泌顆粒に存在するhuman carboxypeptidase H precursor (prohormone processing carboxypeptidase)に比較的高い相同性が見られた。したがって、これらのタンパク質は、分泌タンパク質あるいは膜タンパク質のカテゴリーに入る。

(注5) 5'-端配列データ (one pass sequencing) をもとにクローンを選別したので、PSORTとMEMSATあるいはSOSUIによる全長cDNA配列解析により分泌タンパク質、または膜タンパク質とは予測できないクローンが、6クローン確認された。これらのクローンは、非分泌・非膜タンパク質をコードするものではあるが、「全長率の高いオリゴキャップ法で作成したヒトcDNAライブラリーから、ATGpr等で全長cDNAクローンであると予測されるクローン」としてのカテゴリーに入るものであった。

(注6) PSEC0195と PSEC0206については、機能を予測できる相同性の情報を表

10に示した。他の4クローンは、機能を予測できる相同性やモチーフ情報はなかった。

【0074】

【発明の効果】

本発明により、168種の新規な分泌タンパク質、または膜タンパク質と、それをコードする全長cDNAが提供された。全長cDNAの分離が進んでいないヒトにおいて、新規な全長cDNAを提供した意義は大きい。本発明によって提供される、分泌タンパク質や膜タンパク質は、多くの疾患に関連したタンパク質であることがわかっている。疾患に関連した遺伝子やタンパク質は、診断マーカー、発現や活性を制御する医薬品の開発、あるいは遺伝子治療のターゲットになるなど医薬品の開発等に有効である。中でも、分泌タンパク質をコードするcDNAは、タンパク質自身に医薬品としての有用性が期待できること、および多くの疾患に関連する遺伝子を含む可能性があることから、本発明によって提供されたこれらのcDNAは、産業上きわめて重要である。さらに、膜タンパク質やそれをコードする遺伝子についても、疾患の指標となること等が期待できる。これらのcDNAも、産業上きわめて重要であり、コードするタンパク質の持つ活性の制御や、発現の制御を通じて疾患の治療効果をもたらすこと等が期待される。

【0075】

【配列表】

SEQUENCE LISTING

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55

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Glu Phe Met Asp Asp Ala Asn Met Cys Ile Ala Ile Ala Ile Ser Leu

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80

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Asp Val Met Ser Val Asn Pro Thr Cys Leu Val Leu Ile Ile Leu Leu

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155

160

Phe Ile Ser Ile Ile Leu Thr Phe Lys Gly Tyr Leu Ile Ser Cys Val

165

170

175

Trp Asn Cys Tyr Arg Tyr Ile Asn Gly Arg Asn Ser Ser Asp Val Leu

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185

190

Val Tyr Val Thr Ser Asn Asp Thr Thr Val Leu Leu Pro Pro Tyr Asp

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Asp Ala Thr Val Asn Gly Ala Ala Lys Glu Pro Pro Pro Pro Tyr Val

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Ser Ala

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gga atg gcg cta tcc ggg tcg acc ccg gcc ccg tgc tgg gag gag gat 168

Met Ala Leu Ser Gly Ser Thr Pro Ala Pro Cys Trp Glu Glu Asp

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gag tgc ctg gac tac tac ggg atg ctg tcg ctt cac cgt atg ttc gag 216

Glu Cys Leu Asp Tyr Tyr Gly Met Leu Ser Leu His Arg Met Phe Glu

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gtg gtg ggc ggg caa ctg acc gag tgc gag ctg gag ctc ctg gcc ttt 264

Val Val Gly Gly Gln Leu Thr Glu Cys Glu Leu Glu Leu Leu Ala Phe

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ctg ctg gat gag gct cct ggc gcc gcc gga ggc tta gcc cgg gcc cgc 312

Leu Leu Asp Glu Ala Pro Gly Ala Ala Gly Gly Leu Ala Arg Ala Arg

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agc ggc cta gag ctc ctg ctg gag ctg gag cgc cgc ggg cag tgc ggc 360

Ser Gly Leu Glu Leu Leu Leu Glu Leu Glu Arg Arg Gly Gln Cys Gly

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gag agc aac ctg cgg ctg ctg ggg caa ctc ctg cgc gtg ctg gcc cgc 408

Glu Ser Asn Leu Arg Leu Leu Gly Gln Leu Leu Arg Val Leu Ala Arg

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90

95

cac gac ctg ctg ccg cac ctg gcg cgc aag cgg cgc cgg cca gtg tct 456

His Asp Leu Leu Pro His Leu Ala Arg Lys Arg Arg Arg Pro Val Ser

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105

110

cca gaa cgc tat agc tat ggc acc tcc agc tct tca aag agg aca gag 504

Pro Glu Arg Tyr Ser Tyr Gly Thr Ser Ser Ser Ser Lys Arg Thr Glu

115

120

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ggt agc tgc cgt cgc cgt cgg cag tca agc agt tct gca aat tct cag 552

Gly Ser Cys Arg Arg Arg Arg Gln Ser Ser Ser Ser Ala Asn Ser Gln

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cag ggt cag tgg gag aca ggc tcc ccc cca acc aag cgg cag cgg cgg 600

Gln Gly Gln Trp Glu Thr Gly Ser Pro Pro Thr Lys Arg Gln Arg Arg

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agt cgg ggc cgg ccc agt ggt ggt gcc aga cgg cgg cgg aga ggg gcc 648

Ser Arg Gly Arg Pro Ser Gly Gly Ala Arg Arg Arg Arg Arg Gly Ala

160

165

170

175

cca gcc gca ccc cag cag cag tca gag ccc gcc aga cct tcc tct gaa 696

Pro Ala Ala Pro Gln Gln Gln Ser Glu Pro Ala Arg Pro Ser Ser Glu

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ggc aaa gtg acc tgt gac atc cgg ctc cgg gtt cga gca gag tac tgc 744

Gly Lys Val Thr Cys Asp Ile Arg Leu Arg Val Arg Ala Glu Tyr Cys

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gag cat ggg cca gcc ttg gag cag ggc gtg gca tcc cgg cgg ccc cag 792

Glu His Gly Pro Ala Leu Glu Gln Gly Val Ala Ser Arg Arg Pro Gln

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gcg ctg gcg cgg cag ctg gac gtg ttt ggg cag gcc acc gca gtg ctg 840

Ala Leu Ala Arg Gln Leu Asp Val Phe Gly Gln Ala Thr Ala Val Leu

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cgc tca agg gac ctg ggc tct gtg gtt tgt gac atc aag ttc tca gag 888

Arg Ser Arg Asp Leu Gly Ser Val Val Cys Asp Ile Lys Phe Ser Glu

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ctc tcc tat ctg gac gcc ttc tgg ggc gac tac ctg agt ggc gcc ctg 936

Leu Ser Tyr Leu Asp Ala Phe Trp Gly Asp Tyr Leu Ser Gly Ala Leu

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265

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ctg cag gcc ctg cgg ggc gtg ttc ctg act gag gcc ctg cga gag gct 984

Leu Gln Ala Leu Arg Gly Val Phe Leu Thr Glu Ala Leu Arg Glu Ala

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gtg ggc cgg gag gct gtt cgc ctg ctg gtc agt gtg gat gag gct gac 1032

Val Gly Arg Glu Ala Val Arg Leu Leu Val Ser Val Asp Glu Ala Asp

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295

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tat gag gct ggc cgg cgc cgc ctg ttg ctg atg gag gag gaa ggg ggg 1080

Tyr Glu Ala Gly Arg Arg Arg Leu Leu Leu Met Glu Glu Glu Gly Gly

305

310

315

cgg cgc ccg aca gag gcc tcc tgatccagga ctggcaggat tgatcccacc 1131

Arg Arg Pro Thr Glu Ala Ser

320

325

tccaagtctc cgggccacct tctcctggga ggacgaccat ctctaccct tgacagcccc 1191

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aattaaactg ccctggaaag ggcataggtg gg 1883

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<213> Homo sapiens

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Cys Leu Asp Tyr Tyr Gly Met Leu Ser Leu His Arg Met Phe Glu Val

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Val Gly Gly Gln Leu Thr Glu Cys Glu Leu Glu Leu Leu Ala Phe Leu

35 40 45

Leu Asp Glu Ala Pro Gly Ala Ala Gly Gly Leu Ala Arg Ala Arg Ser

50 55 60

Gly Leu Glu Leu Leu Leu Glu Leu Glu Arg Arg Gly Gln Cys Gly Glu

65 70 75 80

Ser Asn Leu Arg Leu Leu Gly Gln Leu Leu Arg Val Leu Ala Arg His

85

90

95

Asp Leu Leu Pro His Leu Ala Arg Lys Arg Arg Arg Pro Val Ser Pro

100

105

110

Glu Arg Tyr Ser Tyr Gly Thr Ser Ser Ser Ser Lys Arg Thr Glu Gly

115

120

125

Ser Cys Arg Arg Arg Arg Gln Ser Ser Ser Ser Ala Asn Ser Gln Gln

130

135

140

Gly Gln Trp Glu Thr Gly Ser Pro Pro Thr Lys Arg Gln Arg Arg Ser

145

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155

160

Arg Gly Arg Pro Ser Gly Gly Ala Arg Arg Arg Arg Arg Gly Ala Pro

165

170

175

Ala Ala Pro Gln Gln Gln Ser Glu Pro Ala Arg Pro Ser Ser Glu Gly

180

185

190

Lys Val Thr Cys Asp Ile Arg Leu Arg Val Arg Ala Glu Tyr Cys Glu

195

200

205

His Gly Pro Ala Leu Glu Gln Gly Val Ala Ser Arg Arg Pro Gln Ala

210

215

220

Leu Ala Arg Gln Leu Asp Val Phe Gly Gln Ala Thr Ala Val Leu Arg

225

230

235

240

Ser Arg Asp Leu Gly Ser Val Val Cys Asp Ile Lys Phe Ser Glu Leu

245

250

255

Ser Tyr Leu Asp Ala Phe Trp Gly Asp Tyr Leu Ser Gly Ala Leu Leu

260

265

270

Gln Ala Leu Arg Gly Val Phe Leu Thr Glu Ala Leu Arg Glu Ala Val

275

280

285

Gly Arg Glu Ala Val Arg Leu Leu Val Ser Val Asp Glu Ala Asp Tyr

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Glu Ala Gly Arg Arg Arg Leu Leu Leu Met Glu Glu Glu Gly Gly Arg

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315

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Arg Pro Thr Glu Ala Ser

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Met Ala Ser Ala Gly Met Gln Ile Leu Gly Val Val Leu Thr Leu Leu

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ggc tgg gtg aat ggc ctg gtc tcc tgt gcc ctg ccc atg tgg aag gtg 154

Gly Trp Val Asn Gly Leu Val Ser Cys Ala Leu Pro Met Trp Lys Val

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acc gct ttc atc ggc aac agc atc gtg gtg gcc cag gtg gtg tgg gag 202

Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val Val Trp Glu

35 40 45

ggc ctg tgg atg tcc tgc gtg gtg cag agc acc ggc cag atg cag tgc 250

Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys

50 55 60

aag gtg tac gac tca ctg ctg gcg ctg cca cag gac ctg cag gct gca 298

Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala

65 70 75 80

cgt gcc ctc tgt gtc atc gcc ctc ctt gtg gcc ctg ttc ggc ttg ctg 346

Arg Ala Leu Cys Val Ile Ala Leu Leu Val Ala Leu Phe Gly Leu Leu

85 90 95

gtc tac ctt gct ggg gcc aag tgt acc acc tgt gtg gag gag aag gat 394

Val Tyr Leu Ala Gly Ala Lys Cys Thr Thr Cys Val Glu Glu Lys Asp

100 105 110

tcc aag gcc cgc ctg gtg ctc acc tct ggg att gtc ttt gtc atc tca 442
 Ser Lys Ala Arg Leu Val Leu Thr Ser Gly Ile Val Phe Val Ile Ser
 115 120 125

ggg gtc ctg acg cta atc ccc gtg tgc tgg acg gcg cat gcc gtc atc 490
 Gly Val Leu Thr Leu Ile Pro Val Cys Trp Thr Ala His Ala Val Ile
 130 135 140

cgg gac ttc tat aac ccc ctg gtg gct gag gcc caa aag cgg gag ctg 538
 Arg Asp Phe Tyr Asn Pro Leu Val Ala Glu Ala Gln Lys Arg Glu Leu
 145 150 155 160

ggg gcc tcc ctc tac ttg ggc tgg gcg gcc tca ggc ctt ttg ttg ctg 586
 Gly Ala Ser Leu Tyr Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu
 165 170 175

ggg ggg ggg ttg ctg tgc tgc act tgc ccc tcg ggg ggg tcc cag ggc 634
 Gly Gly Gly Leu Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly
 180 185 190

ccc agc cat tac atg gcc cgc tac tca aca tct gcc cct gcc atc tct 682
 Pro Ser His Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser
 195 200 205

cgg ggg ccc tct gag tac cct acc aag aat tac gtc tgacgtggag 728
 Arg Gly Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val
 210 215 220

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gatgggttcg taccttttgt ttctgcctcc tgctattttt cttttgactg aggatattta 848
aaattcattt gaaaactgag ctaaggtggt gactcagact ctcacttagg ctctgctggt 908
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Gly Trp Val Asn Gly Leu Val Ser Cys Ala Leu Pro Met Trp Lys Val
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Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val Val Trp Glu
35 40 45

Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys
50 55 60

Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala
65 70 75 80

Arg Ala Leu Cys Val Ile Ala Leu Leu Val Ala Leu Phe Gly Leu Leu
85 90 95

Val Tyr Leu Ala Gly Ala Lys Cys Thr Thr Cys Val Glu Glu Lys Asp
100 105 110

Ser Lys Ala Arg Leu Val Leu Thr Ser Gly Ile Val Phe Val Ile Ser
115 120 125

Gly Val Leu Thr Leu Ile Pro Val Cys Trp Thr Ala His Ala Val Ile
130 135 140

Arg Asp Phe Tyr Asn Pro Leu Val Ala Glu Ala Gln Lys Arg Glu Leu
145 150 155 160

Gly Ala Ser Leu Tyr Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu
 165 170 175

Gly Gly Gly Leu Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly
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Pro Ser His Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser
 195 200 205

Arg Gly Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val
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<212> DNA

<213> Homo sapiens

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<222> (135)..(1844)

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ttctcgccgc cccg atg gcg ttc cgg ggc tgg agg ccc ccg cca ccg 170

Met Ala Phe Arg Gly Trp Arg Pro Pro Pro Pro Pro

1

5

10

ctg ctc ctg ctg ctg ctc tgg gtg acc ggg cag gca gcg ccc gtg gcg 218

Leu Leu Leu Leu Leu Leu Trp Val Thr Gly Gln Ala Ala Pro Val Ala

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ggc ctg ggc tcc gac gcg gag ctg cag atc gag cgg cgc ttc gtg ccc 266

Gly Leu Gly Ser Asp Ala Glu Leu Gln Ile Glu Arg Arg Phe Val Pro

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gac gag tgc ccg cgc acc gtg cgc agc ggc gac ttc gtg cgc tac cac 314

Asp Glu Cys Pro Arg Thr Val Arg Ser Gly Asp Phe Val Arg Tyr His

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55

60

tac gtg ggg acg ttc ccc gac ggc cag aag ttc gac tcc agc tat gac 362

Tyr Val Gly Thr Phe Pro Asp Gly Gln Lys Phe Asp Ser Ser Tyr Asp

65

70

75

aga gac tcc act ttc aat gtg ttt gtg gga aaa gga cag ctg atc aca 410

Arg Asp Ser Thr Phe Asn Val Phe Val Gly Lys Gly Gln Leu Ile Thr

80

85

90

ggg atg gac cag gct ctt gtt ggg atg tgc gta aac gag aga cgt ttc 458

Gly Met Asp Gln Ala Leu Val Gly Met Cys Val Asn Glu Arg Arg Phe

95

100

105

gtg aag att ccc cca aag ctt gcc tac gga aat gaa gga gtt tct ggt 506

Val Lys Ile Pro Pro Lys Leu Ala Tyr Gly Asn Glu Gly Val Ser Gly

110

115

120

gtg atc ccc ccc aat tca gtg ctt cat ttt gat gta ctt ctg atg gat 554

Val Ile Pro Pro Asn Ser Val Leu His Phe Asp Val Leu Leu Met Asp

125

130

135

140

att tgg aat tct gaa gac cag gtt cag att cac acc tat ttc aag ccc 602

Ile Trp Asn Ser Glu Asp Gln Val Gln Ile His Thr Tyr Phe Lys Pro

145

150

155

ccg agt tgc cct cgg acc atc cag gtg tct gat ttt gtg agg tac cac 650

Pro Ser Cys Pro Arg Thr Ile Gln Val Ser Asp Phe Val Arg Tyr His

160

165

170

tac aac ggg acg ttc ctg gac gga act ctg ttt gat tcg agt cac aat 698

Tyr Asn Gly Thr Phe Leu Asp Gly Thr Leu Phe Asp Ser Ser His Asn

175

180

185

cgc atg aaa aca tat gac acg tat gtg gga att ggc tgg ctg att cct 746

Arg Met Lys Thr Tyr Asp Thr Tyr Val Gly Ile Gly Trp Leu Ile Pro

190

195

200

gga atg gat aaa ggg ctg ctg ggg atg tgt gtg ggt gag aag cgc atc 794

Gly Met Asp Lys Gly Leu Leu Gly Met Cys Val Gly Glu Lys Arg Ile

205

210

215

220

atc acc att cct cct ttt ctg gcc tat gga gag gat gga gat ggg aaa 842

Ile Thr Ile Pro Pro Phe Leu Ala Tyr Gly Glu Asp Gly Asp Gly Lys

225

230

235

gac att ccc ggt cag gca tct ctg gtg ttt gat gtt gca tta ttg gac 890
 Asp Ile Pro Gly Gln Ala Ser Leu Val Phe Asp Val Ala Leu Leu Asp
 240 245 250

ctc cat aac ccc aag gac agc att tcc att gag aac aag gta gta cct 938
 Leu His Asn Pro Lys Asp Ser Ile Ser Ile Glu Asn Lys Val Val Pro
 255 260 265

gaa aac tgt gag cgg ata agt caa agt ggg gac ttt ctc agg tat cat 986
 Glu Asn Cys Glu Arg Ile Ser Gln Ser Gly Asp Phe Leu Arg Tyr His
 270 275 280

tac aat ggc acg ctt ctg gat ggc acc ctc ttt gat tcc agc tac tct 1034
 Tyr Asn Gly Thr Leu Leu Asp Gly Thr Leu Phe Asp Ser Ser Tyr Ser
 285 290 295 300

cgg aac cgc acg ttt gac acg tac att ggg cag ggc tac gtg att cct 1082
 Arg Asn Arg Thr Phe Asp Thr Tyr Ile Gly Gln Gly Tyr Val Ile Pro
 305 310 315

ggg atg gat gaa ggt cta ctt ggt gtt tgc att gga gaa aag cga agg 1130
 Gly Met Asp Glu Gly Leu Leu Gly Val Cys Ile Gly Glu Lys Arg Arg
 320 325 330

att gtg gtc ccg cct cac ctg ggg tat gga gag gaa gga aga ggg aat 1178
 Ile Val Val Pro Pro His Leu Gly Tyr Gly Glu Glu Gly Arg Gly Asn
 335 340 345

atc ccc ggc tgc gct gtg ctg gtg ttt gac atc cat gtg atc gac ttc 1226
 Ile Pro Gly Ser Ala Val Leu Val Phe Asp Ile His Val Ile Asp Phe
 350 355 360

cac aac cct tgc gac tcc atc agc atc acc tcc cac tac aaa ccc cct 1274
 His Asn Pro Ser Asp Ser Ile Ser Ile Thr Ser His Tyr Lys Pro Pro
 365 370 375 380

gac tgc tca gtg ctg agt aag aag gga gat tac ctc aaa tat cac tac 1322
 Asp Cys Ser Val Leu Ser Lys Lys Gly Asp Tyr Leu Lys Tyr His Tyr
 385 390 395

aat gcc tca ctt ctg gat ggg acc ctg ctg gac tcc acg tgg aat tta 1370
 Asn Ala Ser Leu Leu Asp Gly Thr Leu Leu Asp Ser Thr Trp Asn Leu
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ggc aaa act tac aat att gtt ctg gga tct ggg caa gtt gtg ttg ggg 1418
 Gly Lys Thr Tyr Asn Ile Val Leu Gly Ser Gly Gln Val Val Leu Gly
 415 420 425

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Met Asp Met Gly Leu Arg Glu Met Cys Val Gly Glu Lys Arg Thr Val
 430 435 440

atc att ccg cct cac ctg ggc tat ggg gaa gct ggc gtg gat gga gaa 1514
 Ile Ile Pro Pro His Leu Gly Tyr Gly Glu Ala Gly Val Asp Gly Glu
 445 450 455 460

gtg ccc ggc agt gcc gta tta gtg ttt gac att gag ctg ccg gag ctg 1562

Val Pro Gly Ser Ala Val Leu Val Phe Asp Ile Glu Leu Pro Glu Leu

465

470

475

gtg gct ggc ctt cct gag ggg tac atg ttc ata tgg aat ggt gag gtg 1610

Val Ala Gly Leu Pro Glu Gly Tyr Met Phe Ile Trp Asn Gly Glu Val

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485

490

tca ccc aac ctc ttt gaa gaa att gac aag gat ggc aac gga gaa gtc 1658

Ser Pro Asn Leu Phe Glu Glu Ile Asp Lys Asp Gly Asn Gly Glu Val

495

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ctc ctg gaa gag ttc tca gag tac att cac gcc cag gtg gca tct ggc 1706

Leu Leu Glu Glu Phe Ser Glu Tyr Ile His Ala Gln Val Ala Ser Gly

510

515

520

aaa ggg aaa ctc gct cct ggc ttt gat gct gag ctg att gtg aag aat 1754

Lys Gly Lys Leu Ala Pro Gly Phe Asp Ala Glu Leu Ile Val Lys Asn

525

530

535

540

atg ttc acc aac cag gac cgg aat gga gat ggg aag gtc aca gcc gag 1802

Met Phe Thr Asn Gln Asp Arg Asn Gly Asp Gly Lys Val Thr Ala Glu

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550

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gaa ttt aaa ctc aaa gac cag gaa gcc aaa cac gat gaa ctc 1844

Glu Phe Lys Leu Lys Asp Gln Glu Ala Lys His Asp Glu Leu

560

565

570

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3425

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<211> 570

<212> PRT

<213> Homo sapiens

<400> 8

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Leu Leu Trp Val Thr Gly Gln Ala Ala Pro Val Ala Gly Leu Gly Ser

20 25 30

Asp Ala Glu Leu Gln Ile Glu Arg Arg Phe Val Pro Asp Glu Cys Pro

35 40 45

Arg Thr Val Arg Ser Gly Asp Phe Val Arg Tyr His Tyr Val Gly Thr

50 55 60

Phe Pro Asp Gly Gln Lys Phe Asp Ser Ser Tyr Asp Arg Asp Ser Thr

65 70 75 80

Phe Asn Val Phe Val Gly Lys Gly Gln Leu Ile Thr Gly Met Asp Gln

85 90 95

Ala Leu Val Gly Met Cys Val Asn Glu Arg Arg Phe Val Lys Ile Pro

100 105 110

Pro Lys Leu Ala Tyr Gly Asn Glu Gly Val Ser Gly Val Ile Pro Pro

115 120 125

Asn Ser Val Leu His Phe Asp Val Leu Leu Met Asp Ile Trp Asn Ser

130 135 140

Glu Asp Gln Val Gln Ile His Thr Tyr Phe Lys Pro Pro Ser Cys Pro

145 150 155 160

Arg Thr Ile Gln Val Ser Asp Phe Val Arg Tyr His Tyr Asn Gly Thr

165 170 175

Phe Leu Asp Gly Thr Leu Phe Asp Ser Ser His Asn Arg Met Lys Thr

180 185 190

Tyr Asp Thr Tyr Val Gly Ile Gly Trp Leu Ile Pro Gly Met Asp Lys

195 200 205

Gly Leu Leu Gly Met Cys Val Gly Glu Lys Arg Ile Ile Thr Ile Pro

210 215 220

Pro Phe Leu Ala Tyr Gly Glu Asp Gly Asp Gly Lys Asp Ile Pro Gly

225 230 235 240

Gln Ala Ser Leu Val Phe Asp Val Ala Leu Leu Asp Leu His Asn Pro

245 250 255

Lys Asp Ser Ile Ser Ile Glu Asn Lys Val Val Pro Glu Asn Cys Glu

260 265 270

Arg Ile Ser Gln Ser Gly Asp Phe Leu Arg Tyr His Tyr Asn Gly Thr

275 280 285

Leu Leu Asp Gly Thr Leu Phe Asp Ser Ser Tyr Ser Arg Asn Arg Thr

290 295 300

Phe Asp Thr Tyr Ile Gly Gln Gly Tyr Val Ile Pro Gly Met Asp Glu
305 310 315 320

Gly Leu Leu Gly Val Cys Ile Gly Glu Lys Arg Arg Ile Val Val Pro
325 330 335

Pro His Leu Gly Tyr Gly Glu Glu Gly Arg Gly Asn Ile Pro Gly Ser
340 345 350

Ala Val Leu Val Phe Asp Ile His Val Ile Asp Phe His Asn Pro Ser
355 360 365

Asp Ser Ile Ser Ile Thr Ser His Tyr Lys Pro Pro Asp Cys Ser Val
370 375 380

Leu Ser Lys Lys Gly Asp Tyr Leu Lys Tyr His Tyr Asn Ala Ser Leu
385 390 395 400

Leu Asp Gly Thr Leu Leu Asp Ser Thr Trp Asn Leu Gly Lys Thr Tyr
405 410 415

Asn Ile Val Leu Gly Ser Gly Gln Val Val Leu Gly Met Asp Met Gly
420 425 430

Leu Arg Glu Met Cys Val Gly Glu Lys Arg Thr Val Ile Ile Pro Pro
435 440 445

His Leu Gly Tyr Gly Glu Ala Gly Val Asp Gly Glu Val Pro Gly Ser
450 455 460

Ala Val Leu Val Phe Asp Ile Glu Leu Pro Glu Leu Val Ala Gly Leu

465 470 475 480

Pro Glu Gly Tyr Met Phe Ile Trp Asn Gly Glu Val Ser Pro Asn Leu

485 490 495

Phe Glu Glu Ile Asp Lys Asp Gly Asn Gly Glu Val Leu Leu Glu Glu

500 505 510

Phe Ser Glu Tyr Ile His Ala Gln Val Ala Ser Gly Lys Gly Lys Leu

515 520 525

Ala Pro Gly Phe Asp Ala Glu Leu Ile Val Lys Asn Met Phe Thr Asn

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Lys Asp Gln Glu Ala Lys His Asp Glu Leu

565 570

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cct ggg gtc ctg gtg cgg acc ggg cac acc gtg ctg acc tgg gga atc 101

Pro Gly Val Leu Val Arg Thr Gly His Thr Val Leu Thr Trp Gly Ile

10 15 20

acg ctg gtg ctc ttc ctg cac gat acc gag ctg cgg caa tgg gag gag 149

Thr Leu Val Leu Phe Leu His Asp Thr Glu Leu Arg Gln Trp Glu Glu

25 30 35 40

cag ggg gag ctg ctc ctg ccc ctc acc ttc ctg ctc ctg gtg ctg ggc 197

Gln Gly Glu Leu Leu Leu Pro Leu Thr Phe Leu Leu Leu Val Leu Gly

45 50 55

tcc ctg ctg ctc tac ctc gct gtg tca ctc atg gac cct ggc tac gtg 245

Ser Leu Leu Leu Tyr Leu Ala Val Ser Leu Met Asp Pro Gly Tyr Val

60 65 70

aat gtg cag ccc cag cct cag gag gag ctc aaa gag gag cag aca gcc 293

Asn Val Gln Pro Gln Pro Gln Glu Glu Leu Lys Glu Glu Gln Thr Ala

75 80 85

atg gtt cct cca gcc atc cct ctt cgg cgc tgc aga tac tgc ctg gtg 341

Met Val Pro Pro Ala Ile Pro Leu Arg Arg Cys Arg Tyr Cys Leu Val
 90 95 100

ctg cag ccc ctg agg gct cgg cac tgc cgt gag tgc cgc cgt tgc gtc 389
 Leu Gln Pro Leu Arg Ala Arg His Cys Arg Glu Cys Arg Arg Cys Val
 105 110 115 120

cgc cgc tac gac cac cac tgc ccc tgg atg gag aac tgt gtg gga gag 437
 Arg Arg Tyr Asp His His Cys Pro Trp Met Glu Asn Cys Val Gly Glu
 125 130 135

cgc aac cac cca ctc ttt gtg gtc tac ctg gcg ctg cag ctg gtg gtg 485
 Arg Asn His Pro Leu Phe Val Val Tyr Leu Ala Leu Gln Leu Val Val
 140 145 150

ctt ctg tgg ggc ctg tac ctg gca tgg tca ggc ctc cgg ttc ttc cag 533
 Leu Leu Trp Gly Leu Tyr Leu Ala Trp Ser Gly Leu Arg Phe Phe Gln
 155 160 165

ccc tgg ggt ctg tgg ttg cgg tcc agc ggg ctc ctg ttc gcc acc ttc 581
 Pro Trp Gly Leu Trp Leu Arg Ser Ser Gly Leu Leu Phe Ala Thr Phe

170 175 180

ctg ctg ctg tcc cac ttc ttc tgt gga tgg ccc tca ggg tcc tgg gag 629
 Leu Leu Leu Ser His Phe Phe Cys Gly Trp Pro Ser Gly Ser Trp Glu
 185 190 195 200

acc ctc tgg gct gag gag gag gaa gag ggc agc agc cca gct gtt 674
 Thr Leu Trp Ala Glu Glu Glu Glu Gly Ser Ser Pro Ala Val

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210

215

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ctggggtgag cgctcagagg gcctggggcc ctactcctg cccacgcctc ccagacccca 794

gaacggagct tcaagtcaga cagatccctg ccttggtggg cagttctgcc ttccaaggaa 854

gaaggggaag aaaaggacct gtgggtggct caggcccaag cagaccccgg gctccacccc 914

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tctt

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<212> PRT

<213> Homo sapiens

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His Thr Val Leu Thr Trp Gly Ile Thr Leu Val Leu Phe Leu His Asp

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25

30

Thr Glu Leu Arg Gln Trp Glu Glu Gln Gly Glu Leu Leu Leu Pro Leu

35

40

45

Thr Phe Leu Leu Leu Val Leu Gly Ser Leu Leu Leu Tyr Leu Ala Val

50

55

60

Ser Leu Met Asp Pro Gly Tyr Val Asn Val Gln Pro Gln Pro Gln Glu

65

70

75

80

Glu Leu Lys Glu Glu Gln Thr Ala Met Val Pro Pro Ala Ile Pro Leu

85

90

95

Arg Arg Cys Arg Tyr Cys Leu Val Leu Gln Pro Leu Arg Ala Arg His

100

105

110

-Cys Arg Glu Cys Arg Arg Cys Val Arg Arg Tyr Asp His His Cys Pro

115

120

125

Trp Met Glu Asn Cys Val Gly Glu Arg Asn His Pro Leu Phe Val Val

130

135

140

Tyr Leu Ala Leu Gln Leu Val Val Leu Leu Trp Gly Leu Tyr Leu Ala

145

150

155

160

Trp Ser Gly Leu Arg Phe Phe Gln Pro Trp Gly Leu Trp Leu Arg Ser

165

170

175

Ser Gly Leu Leu Phe Ala Thr Phe Leu Leu Leu Ser His Phe Phe Cys

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185

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Gly Trp Pro Ser Gly Ser Trp Glu Thr Leu Trp Ala Glu Glu Glu Glu

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Glu Gly Ser Ser Pro Ala Val

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<213> Homo sapiens

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atg aag ctc tta tct ttg gtg gcc gtg gtc ggg tgt ttg ctg gtg ccc 105

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro

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cca gct gaa gcc aac aag agt tct gaa gat atc cgg tgc aaa tgc atc 153

Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile

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25

30

tgt cca cct tat aga aac atc agt ggg cat att tac aac cag aat gta 201

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val

35

40

45

tcc cag aag gac tgc aac tgc ctg cac gtg gtg gag ccc atg cca gtg 249
 Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
 50 55 60

cct ggc cat gac gtg gag gcc tac tgc ctg ctg tgc gag tgc agg tac 297
 Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
 65 70 75 80

gag gag cgc agc acc acc acc atc aag gtc atc att gtc atc tac ctg 345
 Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
 85 90 95

tcc gtg gtg ggt gcc ctg ttg ctc tac atg gcc ttc ctg atg ctg gtg 393
 Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
 100 105 110

gac cct ctg atc cga aag ccg gat gca tac act gag caa ctg cac aat 441
 Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
 115 120 125

gag gag gag aat gag gat gct cgc tct atg gca gca gct gct gca tcc 489
 Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser
 130 135 140

ctc ggg gga ccc cga gca aac aca gtc ctg gag cgt gtg gaa ggt gcc 537
 Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
 145 150 155 160

cag cag cgg tgg aag ctg cag gtg cag gag cag cgg aag aca gtc ttc 585
Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe

165

170

175

gat cgg cac aag atg ctc agc tagatgggct ggtgtggttg ggtcaaggcc 636
Asp Arg His Lys Met Leu Ser

180

ccaacacccat ggctgccagc ttccaggctg gacaaagcag ggggctactt ctcccttccc 696

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cattaaattg ttttatttct ctc 1499

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Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile

20 25 30

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val

35 40 45

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val

50 55 60

Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr

65

70

75

80

Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu

85

90

95

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val

100

105

110

Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn

115

120

125

Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser

130

135

140

Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala

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Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe

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Asp Arg His Lys Met Leu Ser

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Met Gly Ser Val Leu Gly Leu Cys Ser Met Ala Ser

1

5

10

tgg ata cca tgt ttg tgt gga agt gcc ccg tgt ttg cta tgc cga tgc 160

Trp Ile Pro Cys Leu Cys Gly Ser Ala Pro Cys Leu Leu Cys Arg Cys

15

20

25

tgt cct agt gga aac aac tcc act gta act aga ttg atc tat gca ctt 208

Cys Pro Ser Gly Asn Asn Ser Thr Val Thr Arg Leu Ile Tyr Ala Leu

30

35

40

ttc ttg ctt gtt gga gta tgt gta gct tgt gta atg ttg ata cca gga 256

~~Phe Leu Leu Val Gly Val Cys Val Ala Cys Val Met Leu Ile Pro Gly~~

45

50

55

60

atg gaa gaa caa ctg aat aag att cct gga ttt tgt gag aat gag aaa 304

Met Glu Glu Gln Leu Asn Lys Ile Pro Gly Phe Cys Glu Asn Glu Lys

65

70

75

ggt gtt gtc cct tgt aac att ttg gtt ggc tat aaa gct gta tat cgt 352

Gly Val Val Pro Cys Asn Ile Leu Val Gly Tyr Lys Ala Val Tyr Arg

80

85

90

ttg tgc ttt ggt ttg gct atg tcc tat ctt ctt ctc tct tta cta atg 400
Leu Cys Phe Gly Leu Ala Met Ser Tyr Leu Leu Leu Ser Leu Leu Met
95 100 105

atc aaa gtg aag agt agc agt gat cct aga gct gca gtg cac aat gga 448
Ile Lys Val Lys Ser Ser Ser Asp Pro Arg Ala Ala Val His Asn Gly
110 115 120

ttt tgg ttc ttt aaa ttt gct gca gca att gca att att att ggg gca 496
Phe Trp Phe Phe Lys Phe Ala Ala Ala Ile Ala Ile Ile Ile Gly Ala
125 130 135 140

ttc ttc att cca gaa gga act ttt aca act gtg tgg ttt tat gta ggc 544
Phe Phe Ile Pro Glu Gly Thr Phe Thr Thr Val Trp Phe Tyr Val Gly
145 150 155

atg gca ggt gcc ttt tgt ttc atc ctc ata caa cta gtc tta ctt att 592
Met Ala Gly Ala Phe Cys Phe Ile Leu Ile Gln Leu Val Leu Leu Ile
160 165 170

gat ttt gca cat tca tgg aat gaa tcg tgg gtt gaa aaa atg gaa gaa 640
Asp Phe Ala His Ser Trp Asn Glu Ser Trp Val Glu Lys Met Glu Glu
175 180 185

ggg aac tcg aga tgt tgg tat gca gcc ttg tta tca gct aca gct ctg 688
Gly Asn Ser Arg Cys Trp Tyr Ala Ala Leu Leu Ser Ala Thr Ala Leu
190 195 200

aat tat ctg ctg tct tta gtt gct atc gtc ctg ttc ttt gtc tac tac 736

Asn Tyr Leu Leu Ser Leu Val Ala Ile Val Leu Phe Phe Val Tyr Tyr

205 210 215 220

act cat cca gcc agt tgt tca gaa aac aag gcg ttc atc agt gtc aac 784

Thr His Pro Ala Ser Cys Ser Glu Asn Lys Ala Phe Ile Ser Val Asn

225 230 235

atg ctc ctc tgc gtt ggt gct tct gta atg tct ata ctg cca aaa atc 832

Met Leu Leu Cys Val Gly Ala Ser Val Met Ser Ile Leu Pro Lys Ile

240 245 250

caa gaa tca caa cca aga cct ggt ttg tta cag tct tca gta att cag 880

Gln Glu Ser Gln Pro Arg Pro Gly Leu Leu Gln Ser Ser Val Ile Gln

255 260 265

tct aca caa tgt att tgacatggc agctatgacc aatgaaccag aaacaaattg 935

Ser Thr Gln Cys Ile

270

caaccaagt ctactaagca taattggcta caatacaaca agcactgtcc cacaggaagg 995

gcagtcagtc cagtgggtggc atgctcaagg aattatagga ctaattctct ttttgttg 1055

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aatcttactt gggtagagat ggcctttgcc aacaaagtga actgttttgg ttgttttaaa 2075

ctcatgaagt atgggttcag tggaaatggt tggaactctg aaggatttag acaaggtttt 2135

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tgtgttttac ctctaaataa atgaattcag 3125

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<212> PRT

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<400> 14

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Leu Cys Gly Ser Ala Pro Cys Leu Leu Cys Arg Cys Cys Pro Ser Gly

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Asn Asn Ser Thr Val Thr Arg Leu Ile Tyr Ala Leu Phe Leu Leu Val

35 40 45

Gly Val Cys Val Ala Cys Val Met Leu Ile Pro Gly Met Glu Glu Gln

50 55 60

Leu Asn Lys Ile Pro Gly Phe Cys Glu Asn Glu Lys Gly Val Val Pro

65 70 75 80

Cys Asn Ile Leu Val Gly Tyr Lys Ala Val Tyr Arg Leu Cys Phe Gly

85

90

95

Leu Ala Met Ser Tyr Leu Leu Leu Ser Leu Leu Met Ile Lys Val Lys

100

105

110

Ser Ser Ser Asp Pro Arg Ala Ala Val His Asn Gly Phe Trp Phe Phe

115

120

125

Lys Phe Ala Ala Ala Ile Ala Ile Ile Ile Gly Ala Phe Phe Ile Pro

130

135

140

Glu Gly Thr Phe Thr Thr Val Trp Phe Tyr Val Gly Met Ala Gly Ala

145

150

155

160

Phe Cys Phe Ile Leu Ile Gln Leu Val Leu Leu Ile Asp Phe Ala His

165

170

175

Ser Trp Asn Glu Ser Trp Val Glu Lys Met Glu Glu Gly Asn Ser Arg

180

185

190

Cys Trp Tyr Ala Ala Leu Leu Ser Ala Thr Ala Leu Asn Tyr Leu Leu

195

200

205

Ser Leu Val Ala Ile Val Leu Phe Phe Val Tyr Tyr Thr His Pro Ala

210

215

220

Ser Cys Ser Glu Asn Lys Ala Phe Ile Ser Val Asn Met Leu Leu Cys

225 230 235 240

Val Gly Ala Ser Val Met Ser Ile Leu Pro Lys Ile Gln Glu Ser Gln

245 250 255

Pro Arg Pro Gly Leu Leu Gln Ser Ser Val Ile Gln Ser Thr Gln Cys

260 265 270

Ile

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atg gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc 165

Met Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu

1 5 10 15

ggc ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc tgg aac 213

Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn

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gac cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac 261

Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His

35

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tat gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg 309

Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu

50

55

60

aaa tgt gtt gga ggc aca gct ggt tgt gat tct tat acc cca aaa gtc 357

Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val

65

70

75

80

ata cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa 405

Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu

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90

95

tgt aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg 453

Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val

100

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agc tgt gaa ggc tat gag tcc tct gaa gac cag tat gta cta aga ggt 501

Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly

115

120

125

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Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln

130

135

140

gaa ctg aag gag tct gga aag cag cac ggc ttt gcc tct ttc tct gat 597

Glu Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp

145

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155

160

tat tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg 645

Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu

165

170

175

att acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg 693

Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu

180

185

190

ttc ctg agt gac ggg cag tat tct cct cca ccg tac tct gag tat cct 741

Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro

195

200

205

cca ttt tcc cac cgt tac cag aga ttc acc aac tca gca gga cct cct 789

Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro

210

215

220

ccc cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggc cat 837

Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His

225

230

235

240

ggc gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat 885

Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr

245

250

255

gaa aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata 933

Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile

260

265

270

cta gga tat ttg ttt ggc agc aat aga gcg gca aca ccc ttc tca gac 981

Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp

275

280

285

tcg tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat 1029

Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn

290

295

300

agg gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt 1077

Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys

305

310

315

320

tca aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc 1125

Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr

325

330

335

agg aga cga taaagtagaa agttggagtc aaacactgga tgcagaaatt 1174

Arg Arg Arg

ttggattttt catcactttc tcttttagaaa aaaagtacta cctgttaaca attgggaaaa 1234

ggggatatattc aaaagttctg tgggtgttatg tccagtgtag ctttttgtat tctattattt 1294

gaggctaaaa gttgatgtgt gacaaaatac ttatgtgttg tatgtcagtg taacatgcag 1354

atgtatatgt cagtttttga aagtgatcat tacagtggaa cgctaaaaat acattaattt 1414

ctaaaacctg tgatgcccta agaagcatta agaatgaagg tgttgtacta atagaaacta 1474

agtacagaaa atttcagttt taggtgggtg tagctgatga gttattacct catagagact 1534

ataatatctt atttgggtatt atattatttg atgtttgctg ticttcaaac atttaaata 1594

agctttggac taattatgct aatttgtgag ttctgatcac ttttgagctc tgaagctttg 1654

aatcattcag tggaggagat ggccttctgg taactgaata ttaccttctg taggaaaagg 1714

tagaaaataa gcatctagaa ggttggtgtg aatgactctg tgctggcaaa aatgcttgaa 1774

acctctatat tictttcgtt cataagaggt aaaggtcaaa tttttcaaca aaagtctttt 1834

aataacaaaa gcatgcagtt ctctgtgaaa tctcaaatat tgttgtaata gtctgtttca 1894

atcttaaaaa gaatcaataa aaacaaacaa ggg

1927

<210> 16

<211> 339

<212> PRT

<213> Homo sapiens

<400> 16

Met Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu

1 5 10 15

Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn

20 25 30

Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His

35 40 45

Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu

50 55 60

Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val

65 70 75 80

Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu

85 90 95

Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val

100 105 110

Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly

115 120 125

Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln

130 135 140

Glu Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp

145 150 155 160

Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu

165 170 175

Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu

180 185 190

Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro

195 200 205

Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro

210 215 220

Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His

225 230 235 240

Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr

245 250 255

Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile

260 265 270

Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp

275 280 285

Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn

290 295 300

Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys
305 310 315 320

Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr
325 330 335

Arg Arg Arg

<210> 17

<211> 1483

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70)..(1248)

<400> 17

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ccgcttgga atg gcg cct cct ccg cct tcg ccc caa ctg ctt ctc ctg gca 111

Met Ala Pro Pro Pro Pro Ser Pro Gln Leu Leu Leu Leu Ala

1

5

10

gcc ctc gcg agg ctc ctg ggt ccc agc gag gtg atg gct gga ccg gcg 159

Ala Leu Ala Arg Leu Leu Gly Pro Ser Glu Val Met Ala Gly Pro Ala

15

20

25

30

gag gag gcg gga gcc cat tgt ccc gag agc ctg tgg cct ctg cct ccg 207

Glu Glu Ala Gly Ala His Cys Pro Glu Ser Leu Trp Pro Leu Pro Pro

35

40

45

cag gtg tca cca aga gtg acc tac aca cga gtg agc cca ggg cag gct 255

Gln Val Ser Pro Arg Val Thr Tyr Thr Arg Val Ser Pro Gly Gln Ala

50

55

60

gag gat gtc acc ttc ctc tac cac ccc tgt gcc cat ccc tgg ctg aag 303

Glu Asp Val Thr Phe Leu Tyr His Pro Cys Ala His Pro Trp Leu Lys

65

70

75

ctc cag ctt gcc ctc ctg gcc tat gct tgt atg gct aac cct tcc ctc 351

Leu Gln Leu Ala Leu Leu Ala Tyr Ala Cys Met Ala Asn Pro Ser Leu

80

85

90

acc cct gac ttc agc ctc acg cag gat cgg ccc ctg gtg ctg act gca 399

Thr Pro Asp Phe Ser Leu Thr Gln Asp Arg Pro Leu Val Leu Thr Ala

95

100

105

110

tgg ggg ctg gcg ctg gag atg gcc tgg gta gag cca gcc tgg gct gcc 447

Trp Gly Leu Ala Leu Glu Met Ala Trp Val Glu Pro Ala Trp Ala Ala

115

120

125

cac tgg ctg atg agg agg cgg agg agg aag cag agg aag aag aag gca 495

His Trp Leu Met Arg Arg Arg Arg Arg Lys Gln Arg Lys Lys Lys Ala

130

135

140

tgg atc tac tgt gaa agc ctt tca ggg cct gct ccc tcc gag cca act 543

Trp Ile Tyr Cys Glu Ser Leu Ser Gly Pro Ala Pro Ser Glu Pro Thr

145

150

155

ccc ggt aga ggg agg ctg tgc cga aga ggg tgt gtg cag gcc ctg gct 591

Pro Gly Arg Gly Arg Leu Cys Arg Arg Gly Cys Val Gln Ala Leu Ala

160

165

170

ctg gcc ttt gct ctg cgg agc tgg cgg ccc cct ggc aca gag gtg aca 639

Leu Ala Phe Ala Leu Arg Ser Trp Arg Pro Pro Gly Thr Glu Val Thr

175

180

185

190

tct caa ggg ccc agg cag ccc tct tct agt ggt gcc aag agg cgg agg 687

Ser Gln Gly Pro Arg Gln Pro Ser Ser Ser Gly Ala Lys Arg Arg Arg

195

200

205

ctg cgg gct gcc ctt ggt ccc cag ccc act cgc tca gcc ctg agg ttt 735

Leu Arg Ala Ala Leu Gly Pro Gln Pro Thr Arg Ser Ala Leu Arg Phe

210

215

220

ccc tct gct tcc cca ggg agc ttg aag gcc aag cag tcc atg gcg gga 783

Pro Ser Ala Ser Pro Gly Ser Leu Lys Ala Lys Gln Ser Met Ala Gly

225

230

235

atc cct ggt agg gag agt aat gcc cca tct gtg ccc act gtc tcc ctg 831

Ile Pro Gly Arg Glu Ser Asn Ala Pro Ser Val Pro Thr Val Ser Leu

240

245

250

ctg ccg ggg gcg cct gga ggc aat gcc agc tcc agg aca gag gct cag 879

Leu Pro Gly Ala Pro Gly Gly Asn Ala Ser Ser Arg Thr Glu Ala Gln
255 260 265 270

gtg ccc aac ggg caa ggc agc cca ggg ggc tgt gtc tgt tca agt cag 927
Val Pro Asn Gly Gln Gly Ser Pro Gly Gly Cys Val Cys Ser Ser Gln
275 280 285

gct tcc ccg gcc cct cgc gca gca gcg cct cca cgg gca gcc cgg ggc 975
Ala Ser Pro Ala Pro Arg Ala Ala Ala Pro Pro Arg Ala Ala Arg Gly
290 295 300

ccc acc cca cgc act gaa gag gcc gcc tgg gct gcc atg gcc ctg acc 1023
Pro Thr Pro Arg Thr Glu Glu Ala Ala Trp Ala Ala Met Ala Leu Thr
305 310 315

ttc ctg ctg gtg ctg ctc acc ctg gcc acg ctc tgc aca cgg ctg cac 1071
Phe Leu Leu Val Leu Leu Thr Leu Ala Thr Leu Cys Thr Arg Leu His
320 325 330

aga aac ttc cga cgc ggg gag agc atc tac tgg ggg ccc aca gcg gac 1119
Arg Asn Phe Arg Arg Gly Glu Ser Ile Tyr Trp Gly Pro Thr Ala Asp

335 340 345 350

agc cag gac aca gtg gct gct gtg ctg aag cgg agg ctg ctg cag ccc 1167
Ser Gln Asp Thr Val Ala Ala Val Leu Lys Arg Arg Leu Leu Gln Pro
355 360 365

tcg cgc cgg gtc aag cgc tcg cgc cgg aga ccc ctc ctc ccg ccc acg 1215
Ser Arg Arg Val Lys Arg Ser Arg Arg Arg Pro Leu Leu Pro Pro Thr

370

375

380

ccg gac agc ggc ccg gaa ggc gag agc tcg gag tgacggcctg ggacctgcca 1268

Pro Asp Ser Gly Pro Glu Gly Glu Ser Ser Glu

385

390

ctgtggcgtg cggctcctcc ccgcgccgcg aggccgcgac ctctgccacg tggaccgcgc 1328

gcggggcgct ccctggtggc gatggcgcgg cactggccga gcactgcggg ggctttcctc 1388

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caaaactccg tttctaatta aattatTTTT agtag

1483

<210> 18

<211> 393

<212> PRT

<213> Homo sapiens

<400> 18

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15

Ala Arg Leu Leu Gly Pro Ser Glu Val Met Ala Gly Pro Ala Glu Glu

20

25

30

Ala Gly Ala His Cys Pro Glu Ser Leu Trp Pro Leu Pro Pro Gln Val

35

40

45

Ser Pro Arg Val Thr Tyr Thr Arg Val Ser Pro Gly Gln Ala Glu Asp

50

55

60

Val Thr Phe Leu Tyr His Pro Cys Ala His Pro Trp Leu Lys Leu Gln

65

70

75

80

Leu Ala Leu Leu Ala Tyr Ala Cys Met Ala Asn Pro Ser Leu Thr Pro

85

90

95

Asp Phe Ser Leu Thr Gln Asp Arg Pro Leu Val Leu Thr Ala Trp Gly

100

105

110

Leu Ala Leu Glu Met Ala Trp Val Glu Pro Ala Trp Ala Ala His Trp

115

120

125

Leu Met Arg Arg Arg Arg Arg Lys Gln Arg Lys Lys Lys Ala Trp Ile

130

135

140

Tyr Cys Glu Ser Leu Ser Gly Pro Ala Pro Ser Glu Pro Thr Pro Gly

145

150

155

160

Arg Gly Arg Leu Cys Arg Arg Gly Cys Val Gln Ala Leu Ala Leu Ala

165

170

175

Phe Ala Leu Arg Ser Trp Arg Pro Pro Gly Thr Glu Val Thr Ser Gln

180

185

190

Gly Pro Arg Gln Pro Ser Ser Ser Gly Ala Lys Arg Arg Arg Leu Arg

195

200

205

Ala Ala Leu Gly Pro Gln Pro Thr Arg Ser Ala Leu Arg Phe Pro Ser

210

215

220

Ala Ser Pro Gly Ser Leu Lys Ala Lys Gln Ser Met Ala Gly Ile Pro

225

230

235

240

Gly Arg Glu Ser Asn Ala Pro Ser Val Pro Thr Val Ser Leu Leu Pro

245

250

255

Gly Ala Pro Gly Gly Asn Ala Ser Ser Arg Thr Glu Ala Gln Val Pro

260

265

270

Asn Gly Gln Gly Ser Pro Gly Gly Cys Val Cys Ser Ser Gln Ala Ser

275

280

285

Pro Ala Pro Arg Ala Ala Ala Pro Pro Arg Ala Ala Arg Gly Pro Thr

290

295

300

Pro Arg Thr Glu Glu Ala Ala Trp Ala Ala Met Ala Leu Thr Phe Leu

305

310

315

320

Leu Val Leu Leu Thr Leu Ala Thr Leu Cys Thr Arg Leu His Arg Asn

325

330

335

Phe Arg Arg Gly Glu Ser Ile Tyr Trp Gly Pro Thr Ala Asp Ser Gln

340

345

350

Asp Thr Val Ala Ala Val Leu Lys Arg Arg Leu Leu Gln Pro Ser Arg

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Arg Val Lys Arg Ser Arg Arg Arg Pro Leu Leu Pro Pro Thr Pro Asp

370

375

380

Ser Gly Pro Glu Gly Glu Ser Ser Glu

385

390

<210> 19

<211> 1851

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (171)..(518)

<400> 19

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tggggaggtg cccttaacac caagatttta aaagctccaa tttcagagca agagtcgaaa 120

actcacagat aaagttatag ttatttcagg gttctgaaaa gacgcagaac atg aag 176

Met Lys

1

gga ctc aga agt ctg gca gca aca acc ttg gct ctt ttc ctg gtg ttt 224

Gly Leu Arg Ser Leu Ala Ala Thr Thr Leu Ala Leu Phe Leu Val Phe
5 10 15

gtt ttc ctg gga aac tcc agc tgc gct ccg cag aga ctg ttg gag aga 272
Val Phe Leu Gly Asn Ser Ser Cys Ala Pro Gln Arg Leu Leu Glu Arg
20 25 30

agg aac tgg act cct caa gct atg ctc tac ctg aaa ggg gca cag ggt 320
Arg Asn Trp Thr Pro Gln Ala Met Leu Tyr Leu Lys Gly Ala Gln Gly
35 40 45 50

cgc cgc ttc atc tcc gac cag agc cgg aga aag gac ctc tcc gac cgg 368
Arg Arg Phe Ile Ser Asp Gln Ser Arg Arg Lys Asp Leu Ser Asp Arg
55 60 65

cca ctg ccg gaa aga cga agc cca aat ccc caa cta cta act att ccg 416
Pro Leu Pro Glu Arg Arg Ser Pro Asn Pro Gln Leu Leu Thr Ile Pro
70 75 80

gag gca gca acc atc tta ctg gcg tcc ctt cag aaa tca cca gaa gat 464
Glu Ala Ala Thr Ile Leu Leu Ala Ser Leu Gln Lys Ser Pro Glu Asp

85 90 95

gaa gaa aaa aac ttt gat caa acc aga ttc ctg gaa gac agt ctg ctt 512
Glu Glu Lys Asn Phe Asp Gln Thr Arg Phe Leu Glu Asp Ser Leu Leu
100 105 110

aac tgg tgaaaatata ctggattatg ttttaattatg gttctattct ctttgaaaac 568
Asn Trp

115

atgaaccatg tgaataaaac ctttggaccc ttttattcca tttgtaatct taagaacaca 628

cacagatagt tttattcttt cagaaacaaa atatatatag gatgcttagc tgagaacatc 688

atcttctttc attgcttcag gtccgtgtta gatgaccaa aatgttttca gatcaccttg 748

tgtcttactc ttgagtttct tagaatatct ataattataa ggctgaagac taaagtgttc 808

tttcccttta actatagcca gtacctgtct tgatcttagt tgtgtttttt ttttcattt 868

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atcccatccc caagaatgtg gaaggaaggt gagaaacatg gcaggatggg aaataggaga 988

gtatgactct ctatagctca tccaggagta atcaattaag aagataaatt ggatgactgt 1048

ggagaagctc tgtgatagga acatttcagt gtggttgctg agaggagaca gtcattgagg 1108

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tccatgacca aacagactca acagattcaa gtactctgct tactctaatt gactagactc 1348

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cacatgcaca tatacccaca cagcataca cacatactcc tgtggcaaac ataataatgt 1528

atttatttag aattataata tgaccatcat gtttaattatt tttacctaa tcagagttgt 1588

tattgacaaa tgcataagt ggaaagtatt aattcttatt gtcatcagta tttagccatt 1648

atttagtagc tcaagaatat ctttatgtga atgtctctgt aacttggaat tgcaatttca 1708

ctgtgttaag taatcagaac tctgcttata agatttatct gtatcttggt tcataattta 1768

ataatgaaac taaattcaag ttaatgtaat gttgatctcc gtcgaaaaat aacttgtag 1828

cattaaaata tctgtatggc att 1851

<210> 20

<211> 116

<212> PRT

<213> Homo sapiens

<400> 20

Met Lys Gly Leu Arg Ser Leu Ala Ala Thr Thr Leu Ala Leu Phe Leu

1 5 10 15

Val Phe Val Phe Leu Gly Asn Ser Ser Cys Ala Pro Gln Arg Leu Leu

20 25 30

Glu Arg Arg Asn Trp Thr Pro Gln Ala Met Leu Tyr Leu Lys Gly Ala

35

40

45

Gln Gly Arg Arg Phe Ile Ser Asp Gln Ser Arg Arg Lys Asp Leu Ser

50

55

60

Asp Arg Pro Leu Pro Glu Arg Arg Ser Pro Asn Pro Gln Leu Leu Thr

65

70

75

80

Ile Pro Glu Ala Ala Thr Ile Leu Leu Ala Ser Leu Gln Lys Ser Pro

85

90

95

Glu Asp Glu Glu Lys Asn Phe Asp Gln Thr Arg Phe Leu Glu Asp Ser

100

105

110

Leu Leu Asn Trp

115

<210> 21

<211> 2395

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (25)..(1068)

<400> 21

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Met Ala Ala Ala Leu Gly Pro Leu Gly

1 5

tcg tgg cag cag tgg cgg cga tgt ttg tcg gct cgg gat ggg tcc agg 99

Ser Trp Gln Gln Trp Arg Arg Cys Leu Ser Ala Arg Asp Gly Ser Arg

10 15 20 25

atg tta ctc ctt ctt ctt ttg ttg ggg tct ggg cag ggg cca cag caa 147

Met Leu Leu Leu Leu Leu Leu Leu Gly Ser Gly Gln Gly Pro Gln Gln

30 35 40

gtc ggg gcg ggt caa acg ttc gag tac ttg aaa cgg gag cac tcg ctg 195

Val Gly Ala Gly Gln Thr Phe Glu Tyr Leu Lys Arg Glu His Ser Leu

45 50 55

tcg aag ccc tac cag ggt gtg ggc aca ggc agt tcc tca ctg tgg aat 243

Ser Lys Pro Tyr Gln Gly Val Gly Thr Gly Ser Ser Ser Leu Trp Asn

60 65 70

ctg atg ggc aat gcc atg gtg atg acc cag tat atc cgc ctt acc cca 291

Leu Met Gly Asn Ala Met Val Met Thr Gln Tyr Ile Arg Leu Thr Pro

75 80 85

gat atg caa agt aaa cag ggt gcc ttg tgg aac cgg gtg cca tgt ttc 339

Asp Met Gln Ser Lys Gln Gly Ala Leu Trp Asn Arg Val Pro Cys Phe

90 95 100 105

ctg aga gac tgg gag ttg cag gtg cac ttc aaa atc cat gga caa gga 387
Leu Arg Asp Trp Glu Leu Gln Val His Phe Lys Ile His Gly Gln Gly

110 115 120

aag aag aat ctg cat ggg gat ggc ttg gca atc tgg tac aca aag gat 435
Lys Lys Asn Leu His Gly Asp Gly Leu Ala Ile Trp Tyr Thr Lys Asp

125 130 135

cgg atg cag cca ggg cct gtg ttt gga aac atg gac aaa ttt gtg ggg 483
Arg Met Gln Pro Gly Pro Val Phe Gly Asn Met Asp Lys Phe Val Gly

140 145 150

ctg gga gta ttt gta gac acc tac ccc aat gag gag aag cag caa gag 531
Leu Gly Val Phe Val Asp Thr Tyr Pro Asn Glu Glu Lys Gln Gln Glu

155 160 165

cgg gta ttc ccc tac atc tca gcc atg gtg aac aac ggc tcc ctc agc 579
Arg Val Phe Pro Tyr Ile Ser Ala Met Val Asn Asn Gly Ser Leu Ser

170 175 180 185

~~tat gat cat gag cgg gat ggg cgg cct aca gag ctg gga ggc tgc aca 627~~

Tyr Asp His Glu Arg Asp Gly Arg Pro Thr Glu Leu Gly Gly Cys Thr

190 195 200

gcc att gtc cgc aat ctt cat tac gac acc ttc ctg gtg att cgc tac 675
Ala Ile Val Arg Asn Leu His Tyr Asp Thr Phe Leu Val Ile Arg Tyr

205 210 215

gtc aag agg cat ttg acg ata atg atg gat att gat ggc aag cat gag 723

Val Lys Arg His Leu Thr Ile Met Met Asp Ile Asp Gly Lys His Glu

220

225

230

tgg agg gac tgc att gaa gtg ccc gga gtc cgc ctg ccc cgc ggc tac 771

Trp Arg Asp Cys Ile Glu Val Pro Gly Val Arg Leu Pro Arg Gly Tyr

235

240

245

tac ttc ggc acc tcc tcc atc act ggg gat ctc tca gat aat cat gat 819

Tyr Phe Gly Thr Ser Ser Ile Thr Gly Asp Leu Ser Asp Asn His Asp

250

255

260

265

gtc att tcc ttg aag ttg ttt gaa ctg aca gtg gag aga acc cca gaa 867

Val Ile Ser Leu Lys Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu

270

275

280

gag gaa aag ctc cat cga ggt gtg ttc ttg ccc tca gtg gac aat atg 915

Glu Glu Lys Leu His Arg Gly Val Phe Leu Pro Ser Val Asp Asn Met

285

290

295

aag ctg cct gag atg aca gct cca ctg ccg ccc ctg agt ggc ctg gcc 963

Lys Leu Pro Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala

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305

310

ctc ttc ctc atc gtc ttt ttc tcc ctg gtg ttt tct gta ttt gcc ata 1011

Leu Phe Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile

315

320

325

gtc att ggt atc ata ctc tac aac aaa tgg cag gaa cag agc cga aag 1059

Val Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys

330

335

340

345

cgc ttc tac tgagccctcc tgctgccacc acttttgtga ctgtcaccca 1108

Arg Phe Tyr

tgaggtatgg aaggagcagg cactggcctg agcatgcagc ctggagagtg ttcttgtctc 1168

tagcagctgg ttggggacta tattctgtca ctggagtttt gaatgcaggg accccgcatt 1228

cccatggttg tgcatgggga catctaactc tggctctggga agccaccac cccagggcaa 1288

tgctgctgtg atgtgccttt ccctgcagtc ctcccatgtg ggagcagagg tgtgaagaga 1348

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tgtttgactc agaaggccct tctacttcag ttttgaatcc acaaagaatt aaaaactgg 1468

aacaccacag gctttctgac catccattcg ttgggttttg catttgaccc aacctctgc 1528

ctacctgagg agctttcttt ggaaaccagg atggaaactt ctccctgcc ttaccttct 1588

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ccctagggag atggctttct gctttggatc actgttcct agcatgggtc ttgggtctat 1768

tggcatgtcc atggccttcc caatcaagtc tcttcaggcc ctgagttaag ttggctaaa 1828

ggttgggtgta aaaatcaaga gaagcctgga agacatcatg gatgccatgg attagctgtg 1888
 caactgacca gctccagggtt tgatcaaacc aaaagcaaca tttgtcatgt ggtctgacca 1948
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 gaaattctta aaatcaccca tggaacc 2395

<210> 22

<211> 348

<212> PRT

<213> Homo sapiens

<400> 22

Met Ala Ala Ala Leu Gly Pro Leu Gly Ser Trp Gln Gln Trp Arg Arg

1

5

10

15

Cys Leu Ser Ala Arg Asp Gly Ser Arg Met Leu Leu Leu Leu Leu Leu

20

25

30

Leu Gly Ser Gly Gln Gly Pro Gln Gln Val Gly Ala Gly Gln Thr Phe

35

40

45

Glu Tyr Leu Lys Arg Glu His Ser Leu Ser Lys Pro Tyr Gln Gly Val

50

55

60

Gly Thr Gly Ser Ser Ser Leu Trp Asn Leu Met Gly Asn Ala Met Val

65

70

75

80

Met Thr Gln Tyr Ile Arg Leu Thr Pro Asp Met Gln Ser Lys Gln Gly

85

90

95

Ala Leu Trp Asn Arg Val Pro Cys Phe Leu Arg Asp Trp Glu Leu Gln

100

105

110

Val His Phe Lys Ile His Gly Gln Gly Lys Lys Asn Leu His Gly Asp

115

120

125

Gly Leu Ala Ile Trp Tyr Thr Lys Asp Arg Met Gln Pro Gly Pro Val

130

135

140

Phe Gly Asn Met Asp Lys Phe Val Gly Leu Gly Val Phe Val Asp Thr

145

150

155

160

Tyr Pro Asn Glu Glu Lys Gln Gln Glu Arg Val Phe Pro Tyr Ile Ser

165

170

175

Ala Met Val Asn Asn Gly Ser Leu Ser Tyr Asp His Glu Arg Asp Gly

180

185

190

Arg Pro Thr Glu Leu Gly Gly Cys Thr Ala Ile Val Arg Asn Leu His

195

200

205

Tyr Asp Thr Phe Leu Val Ile Arg Tyr Val Lys Arg His Leu Thr Ile

210

215

220

Met Met Asp Ile Asp Gly Lys His Glu Trp Arg Asp Cys Ile Glu Val

225

230

235

240

Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr Phe Gly Thr Ser Ser Ile

245

250

255

Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys Leu Phe

260

265

270

Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu Lys Leu His Arg Gly

275

280

285

Val Phe Leu Pro Ser Val Asp Asn Met Lys Leu Pro Glu Met Thr Ala

290

295

300

Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe Leu Ile Val Phe Phe

305

310

315

320

Ser Leu Val Phe Ser Val Phe Ala Ile Val Ile Gly Ile Ile Leu Tyr

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Asn Lys Trp Gln Glu Gln Ser Arg Lys Arg Phe Tyr

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<210> 23

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<213> Homo sapiens

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atg aaa ttt ctt ctg gac atc ctc ctg ctt ctc ccg tta ctg atc gtc 165

Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu Leu Ile Val

1

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15

tgc tcc cta gag tcc ttc gtg aag ctt ttt att cct aag agg aga aaa 213

Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys

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25

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tca gtc acc ggc gaa acc gtg ctg att aca gga gct ggg cat gga att 261
Ser Val Thr Gly Glu Thr Val Leu Ile Thr Gly Ala Gly His Gly Ile

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ggg aga ctg act gcc tat gaa ttt gct aaa ctt aaa agc aag ctg gtt 309
Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val

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ctc tgg gat ata aat aag cat gga ctg gag gaa aca gct gcc aaa tgc 357
Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys

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70

75

80

aag gga ctg ggt gcc aag gtt cat acc ttt gtg gta gac tgc agc aac 405
Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn

85

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95

cga gaa gat att tac agc tct gca aag aag gtg aag gca gaa att gga 453
Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly

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105

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gat gtt agt att tta gta aat aat gct ggt gta gtc tat aca tca gat 501

Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp

115

120

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ttg ttt gct aca caa gat cct cag att gaa aag act ttt gaa gtt aat 549
Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn

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gta ctt gca cat ttc tgg act aca aag gca ttt ctt cct gca atg acg 597

Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr
145 150 155 160

aag aat aac cat ggc cat att gtc act gtg gct tcg gca gct gga cat 645
Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His
165 170 175

gtc tcg gtc ccc ttc tta ctg gct tac tgt tca agc aag ttt gct gct 693
Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala
180 185 190

gtt gga ttt cat aaa act ttg aca gat gaa ctg gct gcc tta caa ata 741
Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile
195 200 205

act gga gtc aaa aca aca tgt ctg tgt cct aat ttc gta aac act ggc 789
Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly
210 215 220

ttc atc aaa aat cca agt aca agt ttg gga ccc act ctg gaa cct gag 837
Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu
225 230 235 240

gaa gtg gta aac agg ctg atg cat ggg att ctg act gag cag aag atg 885
Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met
245 250 255

att ttt att cca tct tct ata gct ttt tta aca aca ttg gaa agg atc 933
Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile

260

265

270

ctt cct gag cgt ttc ctg gca gtt tta aaa cga aaa atc agt gtt aag 981

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys

275

280

285

ttt gat gca gtt att gga tat aaa atg aaa gcg caa taagcaccta 1027

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln

290

295

300

gttttctgaa aactgattta ccaggttttag gttgatgtca tctaatagtg ccagaatttt 1087

aatgtttgaa ctctgtttt ttctaattat cccatttct tcaatatcat ttttgaggct 1147

ttggcagtct tcatttacta ccacttgttc tttagccaaa agctgattac atatgatata 1207

aacagagaaa tacctttaga ggtgacttta aggaaaatga agaaaaagaa ccaaaatgac 1267

tttattaaaa taatttccaa gattatttgt ggctcacctg aaggctttgc aaaatttgta 1327

ccataaccgt ttatttaaca tatattttta ttttgattg cacttaaatt ttgtataatt 1387

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cctacccatt gccactctgt ttccctgagag atacctcaca ttccaatgcc aaacatttct 1567

gcacagggaa gctagagggtg gatacacgtg ttgcaagtat aaaagcatca ctgggattta 1627

aggagaattg agagaatgta cccacaaatg gcagcaataa taaatggatc acactt 1683

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<212> PRT

<213> Homo sapiens

<400> 24

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Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys

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Ser Val Thr Gly Glu Thr Val Leu Ile Thr Gly Ala Gly His Gly Ile

35 40 45

Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val

50 55 60

Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys

65 70 75 80

Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn

85 90 95

Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly

100

105

110

Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp

115

120

125

Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn

130

135

140

Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr

145

150

155

160

Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His

165

170

175

Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala

180

185

190

Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile

195

200

205

Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly

210

215

220

Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu

225

230

235

240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met

245

250

255

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile
 260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys
 275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
 290 295 300

<210> 25

<211> 1584

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (14)..(1231)

<400> 25

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Met Arg Gly Ser Val Glu Cys Thr Trp Gly Trp Gly

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His Cys Ala Pro Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala

15

20

25

gcc cca ttt ggc ctg ctg ggg gag aag acc cgc cag gtg tct ctg gag 145

Ala Pro Phe Gly Leu Leu Gly Glu Lys Thr Arg Gln Val Ser Leu Glu

30 35 40

gtc atc cct aac tgg ctg ggc ccc ctg cag aac ctg ctt cat ata cgg 193

Val Ile Pro Asn Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg

45 50 55 60

gca gtg ggc acc aat tcc aca ctg cac tat gtg tgg agc agc ctg ggg 241

Ala Val Gly Thr Asn Ser Thr Leu His Tyr Val Trp Ser Ser Leu Gly

65 70 75

cct ctg gca gtg gta atg gtg gcc acc aac acc ccc cac agc acc ctg 289

Pro Leu Ala Val Val Met Val Ala Thr Asn Thr Pro His Ser Thr Leu

80 85 90

agc gtc aac tgg agc ctc ctg cta tcc cct gag ccc gat ggg ggc ctg 337

Ser Val Asn Trp Ser Leu Leu Leu Ser Pro Glu Pro Asp Gly Gly Leu

95 100 105

atg gtg ctc cct aag gac agc att cag ttt tct tct gcc ctt gtt ttt 385

~~Met Val Leu Pro Lys Asp Ser Ile Gln Phe Ser Ser Ala Leu Val Phe~~

110 115 120

acc agg ctg ctt gag ttt gac agc acc aac gtg tcc gat acg gca gca 433

Thr Arg Leu Leu Glu Phe Asp Ser Thr Asn Val Ser Asp Thr Ala Ala

125 130 135 140

aag cct ttg gga aga cca tat cct cca tac tcc ttg gcc gat ttc tct 481

Lys Pro Leu Gly Arg Pro Tyr Pro Pro Tyr Ser Leu Ala Asp Phe Ser

145	150	155	
tgg aac aac atc act gat tca ttg gat cct gcc acc ctg agt gcc aca			529
Trp Asn Asn Ile Thr Asp Ser Leu Asp Pro Ala Thr Leu Ser Ala Thr			
160	165	170	
ttt caa ggc cac ccc atg aac gac cct acc agg act ttt gcc aat ggc			577
Phe Gln Gly His Pro Met Asn Asp Pro Thr Arg Thr Phe Ala Asn Gly			
175	180	185	
agc ctg gcc ttc agg gtc cag gcc ttt tcc agg tcc agc cga cca gcc			625
Ser Leu Ala Phe Arg Val Gln Ala Phe Ser Arg Ser Ser Arg Pro Ala			
190	195	200	
caa ccc cct cgc ctc ctg cac aca gca gac acc tgt cag cta gag gtg			673
Gln Pro Pro Arg Leu Leu His Thr Ala Asp Thr Cys Gln Leu Glu Val			
205	210	215	220
gcc ctg att gga gcc tct ccc cgg gga aac cgt tcc ctg ttt ggg ctg			721
Ala Leu Ile Gly Ala Ser Pro Arg Gly Asn Arg Ser Leu Phe Gly Leu			
225	230	235	
gag gta gcc aca ttg ggc cag ggc cct gac tgc ccc tca atg cag gag			769
Glu Val Ala Thr Leu Gly Gln Gly Pro Asp Cys Pro Ser Met Gln Glu			
240	245	250	
cag cac tcc atc gac gat gaa tat gca ccg gcc gtc ttc cag ttg gac			817
Gln His Ser Ile Asp Asp Glu Tyr Ala Pro Ala Val Phe Gln Leu Asp			
255	260	265	

cag cta ctg tgg ggc tcc ctc cca tca ggc ttt gca cag tgg cga cca 865

Gln Leu Leu Trp Gly Ser Leu Pro Ser Gly Phe Ala Gln Trp Arg Pro

270

275

280

gtg gct tac tcc cag aag ccg ggg ggc cga gaa tca gcc ctg ccc tgc 913

Val Ala Tyr Ser Gln Lys Pro Gly Gly Arg Glu Ser Ala Leu Pro Cys

285

290

295

300

caa gct tcc cct ctt cat cct gcc tta gca tac tct ctt ccc cag tca 961

Gln Ala Ser Pro Leu His Pro Ala Leu Ala Tyr Ser Leu Pro Gln Ser

305

310

315

ccc att gtc cga gcc ttc ttt ggg tcc cag aat aac ttc tgt gcc ttc 1009

Pro Ile Val Arg Ala Phe Phe Gly Ser Gln Asn Asn Phe Cys Ala Phe

320

325

330

aat ctg acg ttc ggg gct tcc aca ggc cct ggc tat tgg gac caa cac 1057

Asn Leu Thr Phe Gly Ala Ser Thr Gly Pro Gly Tyr Trp Asp Gln His

335

340

345

tac ctc agc tgg tgc atg ctc ctt ggt gtg ggc ttc cct cca gtg gac 1105

Tyr Leu Ser Trp Ser Met Leu Leu Gly Val Gly Phe Pro Pro Val Asp

350

355

360

ggc ttg tcc cca cta gtc ctg ggc atc atg gca gtg gcc ctg ggt gcc 1153

Gly Leu Ser Pro Leu Val Leu Gly Ile Met Ala Val Ala Leu Gly Ala

365

370

375

380

cca ggg ctc atg ctg cta ggg ggc ggc ttg gtt ctg ctg ctg cac cac 1201

Pro Gly Leu Met Leu Leu Gly Gly Gly Leu Val Leu Leu Leu His His

385

390

395

aag aag tac tca gag tac cag tcc ata aat taaggccgc tctctggagg 1251

Lys Lys Tyr Ser Glu Tyr Gln Ser Ile Asn

400

405

gaaggacatt actgaacctg tcttgctgtg cctcgaaact ctggagggtg gagcatcaag 1311

ttccagccgg ccccttcaact ccccatctt gcttttctgt ggaacctcag aggccagcct 1371

cgacttcctg gagaccccca ggtggggcctt ccttcataact ttgttggggg actttggagg 1431

cgggcagggg acagggtat tgataagggtc cccttggtgt tgccttcttg catctccaca 1491

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1584

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<211> 406

<212> PRT

<213> Homo sapiens

<400> 26

Met Arg Gly Ser Val Glu Cys Thr Trp Gly Trp Gly His Cys Ala Pro

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Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly

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25

30

Leu Leu Gly Glu Lys Thr Arg Gln Val Ser Leu Glu Val Ile Pro Asn

35

40

45

Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Ala Val Gly Thr

50

55

60

Asn Ser Thr Leu His Tyr Val Trp Ser Ser Leu Gly Pro Leu Ala Val

65

70

75

80

Val Met Val Ala Thr Asn Thr Pro His Ser Thr Leu Ser Val Asn Trp

85

90

95

Ser Leu Leu Leu Ser Pro Glu Pro Asp Gly Gly Leu Met Val Leu Pro

100

105

110

Lys Asp Ser Ile Gln Phe Ser Ser Ala Leu Val Phe Thr Arg Leu Leu

115

120

125

Glu Phe Asp Ser Thr Asn Val Ser Asp Thr Ala Ala Lys Pro Leu Gly

130

135

140

Arg Pro Tyr Pro Pro Tyr Ser Leu Ala Asp Phe Ser Trp Asn Asn Ile

145

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155

160

Thr Asp Ser Leu Asp Pro Ala Thr Leu Ser Ala Thr Phe Gln Gly His

165

170

175

Pro Met Asn Asp Pro Thr Arg Thr Phe Ala Asn Gly Ser Leu Ala Phe

180

185

190

Arg Val Gln Ala Phe Ser Arg Ser Ser Arg Pro Ala Gln Pro Pro Arg

195

200

205

Leu Leu His Thr Ala Asp Thr Cys Gln Leu Glu Val Ala Leu Ile Gly

210

215

220

Ala Ser Pro Arg Gly Asn Arg Ser Leu Phe Gly Leu Glu Val Ala Thr

225

230

235

240

Leu Gly Gln Gly Pro Asp Cys Pro Ser Met Gln Glu Gln His Ser Ile

245

250

255

Asp Asp Glu Tyr Ala Pro Ala Val Phe Gln Leu Asp Gln Leu Leu Trp

260

265

270

Gly Ser Leu Pro Ser Gly Phe Ala Gln Trp Arg Pro Val Ala Tyr Ser

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Gln Lys Pro Gly Gly Arg Glu Ser Ala Leu Pro Cys Gln Ala Ser Pro

290

295

300

Leu His Pro Ala Leu Ala Tyr Ser Leu Pro Gln Ser Pro Ile Val Arg

305

310

315

320

Ala Phe Phe Gly Ser Gln Asn Asn Phe Cys Ala Phe Asn Leu Thr Phe

325

330

335

Gly Ala Ser Thr Gly Pro Gly Tyr Trp Asp Gln His Tyr Leu Ser Trp

340

345

350

Ser Met Leu Leu Gly Val Gly Phe Pro Pro Val Asp Gly Leu Ser Pro

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360

365

Leu Val Leu Gly Ile Met Ala Val Ala Leu Gly Ala Pro Gly Leu Met

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Leu Leu Gly Gly Gly Leu Val Leu Leu Leu His His Lys Lys Tyr Ser

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400

Glu Tyr Gln Ser Ile Asn

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<210> 27

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<212> DNA

<213> Homo sapiens

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<222> (94)..(501)

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Met Gly Ser Leu Tyr Met Phe

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gtt cag acc atc ctt tcc tac caa atg cag ccc aaa atc cat ggc aaa 162

Val Gln Thr Ile Leu Ser Tyr Gln Met Gln Pro Lys Ile His Gly Lys

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caa gtc ttc tgg atc aga ctg ttg ttg gtt atc tgg tgt gga gta agt 210

Gln Val Phe Trp Ile Arg Leu Leu Leu Val Ile Trp Cys Gly Val Ser

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gca ctt agc atg ctg act tgc tca tca gtt ttg cac agt ggc aat ttt 258

Ala Leu Ser Met Leu Thr Cys Ser Ser Val Leu His Ser Gly Asn Phe

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ggg act gat tta gaa cag aaa ctc cat tgg aac ccc gag gac aaa ggt 306

Gly Thr Asp Leu Glu Gln Lys Leu His Trp Asn Pro Glu Asp Lys Gly

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65

70

tat gtg ctt cac atg atc act act gca gca gaa tgg tct atg tca ttt 354

Tyr Val Leu His Met Ile Thr Thr Ala Ala Glu Trp Ser Met Ser Phe

75

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85

tcc ttc ttt ggt ttt ttc ctg act tac att cgt gat ttt cag aaa att 402

Ser Phe Phe Gly Phe Phe Leu Thr Tyr Ile Arg Asp Phe Gln Lys Ile

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95

100

tct tta cgg gtg gaa gcc aat tta cat gga tta acc ctc tat gac act 450

Ser Leu Arg Val Glu Ala Asn Leu His Gly Leu Thr Leu Tyr Asp Thr

105

110

115

gca cct tgc cct att aac aat gaa cga aca cgg cta ctt tcc aga gat 498

Ala Pro Cys Pro Ile Asn Asn Glu Arg Thr Arg Leu Leu Ser Arg Asp

120

125

130

135

att tgatgaaagg ataaaatatt tctgtaatga ttatgattct cagggattgg 551

Ile

ggaaaggttc acagaagttg cttatttttc tctgaaattt tcaaccactt aatcaaggct 611

gacagtaaca ctgatgaatg ctgataatca ggaaacatga aagaagccat ttgatagatt 671

attctaaagg atatcatcaa gaagactatt aaaaacacct atgcctatac ttttttatct 731

cagaaaataa agtcaaaaga ctatgatatc atagttttta taccttattt aaggaggaaa 791

~~caacctgacg tggcaccaat cagttctggc acatcccaac ccttcacatt ttataaatta 851~~

ttgtagatca tgttttgtta ggagcacttt tatgagagac attttccatg actaaataat 911

cagcattagt cagtaaatec tttagaactg ggttttgaaa tgggagtttt atcatattaa 971

atcatttctt gtagtcttac attttttggtt gttgttctgg aatctacctg taaaggaaag 1031

tagacctgga ttcatgtggg ctcttccatg gcttaagtgt tgcccaagag atttttagg 1091

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aggagagagg cacctgtagg taaatttact ttagtcatat tttatataaa acaagggtta 1271

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accat 1336

<210> 28

<211> 136

<212> PRT

<213> Homo sapiens

<400> 28

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Gln Pro Lys Ile His Gly Lys Gln Val Phe Trp Ile Arg Leu Leu Leu

20 25 30

Val Ile Trp Cys Gly Val Ser Ala Leu Ser Met Leu Thr Cys Ser Ser

35 40 45

Val Leu His Ser Gly Asn Phe Gly Thr Asp Leu Glu Gln Lys Leu His

50 55 60

Trp Asn Pro Glu Asp Lys Gly Tyr Val Leu His Met Ile Thr Thr Ala
65 70 75 80

Ala Glu Trp Ser Met Ser Phe Ser Phe Phe Gly Phe Phe Leu Thr Tyr
85 90 95

Ile Arg Asp Phe Gln Lys Ile Ser Leu Arg Val Glu Ala Asn Leu His
100 105 110

Gly Leu Thr Leu Tyr Asp Thr Ala Pro Cys Pro Ile Asn Asn Glu Arg
115 120 125

Thr Arg Leu Leu Ser Arg Asp Ile
130 135

<210> 29

<211> 1729

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (29)..(1246)

<400> 29

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Met Gly Pro Ser Thr Pro Leu Leu

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Ile Leu Phe Leu Leu Ser Trp Ser Gly Pro Leu Gln Gly Gln Gln His

10

15

20

cac ctt gtg gag tac atg gaa cgc cga cta gct gct tta gag gaa cgg 148

His Leu Val Glu Tyr Met Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg

25

30

35

40

ctg gcc cag tgc cag gac cag agt agt cgg cat gct gct gag ctg cgg 196

Leu Ala Gln Cys Gln Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg

45

50

55

gac ttc aag aac aag atg ctg cca ctg ctg gag gtg gca gag aag gag 244

Asp Phe Lys Asn Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu

60

65

70

cgg gag gca ctc aga act gag gcc gac acc atc tcc ggg aga gtg gat 292

Arg Glu Ala Leu Arg Thr Glu Ala Asp Thr Ile Ser Gly Arg Val Asp

75

80

85

cgt ctg gag cgg gag gta gac tat ctg gag acc cag aac cca gct ctg 340

Arg Leu Glu Arg Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu

90

95

100

ccc tgt gta gag ttt gat gag aag gtg act gga ggc cct ggg acc aaa 388

Pro Cys Val Glu Phe Asp Glu Lys Val Thr Gly Gly Pro Gly Thr Lys

105

110

115

120

ggc aag gga aga agg aat gag aag tac gat atg gtg aca gac tgt ggc 436
 Gly Lys Gly Arg Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys Gly
 125 130 135

tac aca atc tct caa gtg aga tca atg aag att ctg aag cga ttt ggt 484
 Tyr Thr Ile Ser Gln Val Arg Ser Met Lys Ile Leu Lys Arg Phe Gly
 140 145 150

ggc cca gct ggt cta tgg acc aag gat cca ctg ggg caa aca gag aag 532
 Gly Pro Ala Gly Leu Trp Thr Lys Asp Pro Leu Gly Gln Thr Glu Lys
 155 160 165

atc tac gtg tta gat ggg aca cag aat gac aca gcc ttt gtc ttc cca 580
 Ile Tyr Val Leu Asp Gly Thr Gln Asn Asp Thr Ala Phe Val Phe Pro
 170 175 180

agg ctg cgt gac ttc acc ctt gcc atg gct gcc cgg aaa gct tcc cga 628
 Arg Leu Arg Asp Phe Thr Leu Ala Met Ala Ala Arg Lys Ala Ser Arg
 185 190 195 200

gtc cgg gtg ccc ttc ccc tgg gta ggc aca ggg cag ctg gta tat ggt 676
 Val Arg Val Pro Phe Pro Trp Val Gly Thr Gly Gln Leu Val Tyr Gly
 205 210 215

ggc ttt ctt tat ttt gct cgg agg cct cct gga aga cct ggt gga ggt 724
 Gly Phe Leu Tyr Phe Ala Arg Arg Pro Pro Gly Arg Pro Gly Gly Gly
 220 225 230

ggt gag atg gag aac act ttg cag cta atc aaa ttc cac ctg gca aac 772

Gly Glu Met Glu Asn Thr Leu Gln Leu Ile Lys Phe His Leu Ala Asn

235

240

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cga aca gtg gtg gac agc tca gta ttc cca gca gag ggg ctg atc ccc 820

Arg Thr Val Val Asp Ser Ser Val Phe Pro Ala Glu Gly Leu Ile Pro

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ccc tac ggc ttg aca gca gac acc tac atc gac ctg gca gct gat gag 868

Pro Tyr Gly Leu Thr Ala Asp Thr Tyr Ile Asp Leu Ala Ala Asp Glu

265

270

275

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gaa ggt ctt tgg gct gtc tat gcc acc cgg gag gat gac agg cac ttg 916

Glu Gly Leu Trp Ala Val Tyr Ala Thr Arg Glu Asp Asp Arg His Leu

285

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tgt ctg gcc aag tta gat cca cag aca ctg gac aca gag cag cag tgg 964

Cys Leu Ala Lys Leu Asp Pro Gln Thr Leu Asp Thr Glu Gln Gln Trp

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gac aca cca tgt ccc aga gag aat gct gag gct gcc ttt gtc atc tgt 1012

Asp Thr Pro Cys Pro Arg Glu Asn Ala Glu Ala Ala Phe Val Ile Cys

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Gly Thr Leu Tyr Val Val Tyr Asn Thr Arg Pro Ala Ser Arg Ala Arg

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atc cag tgc tcc ttt gat gcc agc ggc acc ctg acc cct gaa cgg gca 1108

Ile Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala
345 350 355 360

gca ctc cct tat ttt ccc cgc aga tat ggt gcc cat gcc agc ctc cgc 1156
Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu Arg
365 370 375

tat aac ccc cga gaa cgc cag ctc tat gcc tgg gat gat ggc tac cag 1204
Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly Tyr Gln
380 385 390

att gtc tat aag ctg gag atg agg aag aaa gag gag gag gtt 1246
Ile Val Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu Val
395 400 405

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1729

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<213> Homo sapiens

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Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg

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25

30

Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln Asp Gln Ser

35

40

45

Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn Lys Met Leu Pro

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Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala Leu Arg Thr Glu Ala

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75

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Asp Thr Ile Ser Gly Arg Val Asp Arg Leu Glu Arg Glu Val Asp Tyr

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Leu Glu Thr Gln Asn Pro Ala Leu Pro Cys Val Glu Phe Asp Glu Lys

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Val Thr Gly Gly Pro Gly Thr Lys Gly Lys Gly Arg Arg Asn Glu Lys

115

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125

Tyr Asp Met Val Thr Asp Cys Gly Tyr Thr Ile Ser Gln Val Arg Ser

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135

140

Met Lys Ile Leu Lys Arg Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys

145

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155

160

Asp Pro Leu Gly Gln Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln

165

170

175

Asn Asp Thr Ala Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala

180

185

190

Met Ala Ala Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val

195

200

205

Gly Thr Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg

210

215

220

Pro Pro Gly Arg Pro Gly Gly Gly Gly Glu Met Glu Asn Thr Leu Gln

225

230

235

240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser Val

245

250

255

Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala Asp Thr

260

265

270

Tyr Ile Asp Leu Ala Ala Asp Glu Gly Leu Trp Ala Val Tyr Ala

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Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys Leu Asp Pro Gln

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Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro Cys Pro Arg Glu Asn

305

310

315

320

Ala Glu Ala Ala Phe Val Ile Cys Gly Thr Leu Tyr Val Val Tyr Asn

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Thr Arg Pro Ala Ser Arg Ala Arg Ile Gln Cys Ser Phe Asp Ala Ser

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Gly Thr Leu Thr Pro Glu Arg Ala Ala Leu Pro Tyr Phe Pro Arg Arg

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Tyr Gly Ala His Ala Ser Leu Arg Tyr Asn Pro Arg Glu Arg Gln Leu

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Leu Cys Phe Ser Leu Gln Asn Ile Phe Ser Lys Lys Val Leu Arg Asp

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Ser Arg Ile His His Leu Arg Leu Leu Asn Ile Leu Gly Cys His Ala

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Val Phe Phe Met Ile Pro Thr Trp Val Leu Val Asp Leu Ser Ala Phe

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 60 65 70 75

ctg ctc ctg gct gtc agc ggc ttc tgt aac ttt gcc cag aat gtt atc 291
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 Asn Ala Thr Lys Arg Ile Met Val Ile Thr Val Ser Leu Ile Met Leu
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 Arg Asn Pro Val Thr Ser Thr Ile Val Leu Gly Met Met Thr Ala Ile
 125 130 135

ctg ggg gtc ttc ctc tat aac aag acc aag tac gat gca aac cag caa 483
 Leu Gly Val Phe Leu Tyr Asn Lys Thr Lys Tyr Asp Ala Asn Gln Gln
 140 145 150 155

gcc agg aag cac ctc ctc ccc gtc acc aca gca gac ctg agc agc aag 531
 Ala Arg Lys His Leu Leu Pro Val Thr Thr Ala Asp Leu Ser Ser Lys
 160 165 170

gag cgt cac cgg agc cca ctg gag aag ccc cac aac ggc ctc ctc ttc 579

Glu Arg His Arg Ser Pro Leu Glu Lys Pro His Asn Gly Leu Leu Phe

175

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ccc cag cac ggg gac tat cag tac ggc cgc aac aac atc tta aca gac 627

Pro Gln His Gly Asp Tyr Gln Tyr Gly Arg Asn Asn Ile Leu Thr Asp

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His Phe Gln Tyr Ser Arg Gln Ser Tyr Pro Asn Ser Tyr Ser Leu Asn

205

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Arg Tyr Asp Val

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35 40 45

Pro Thr Trp Val Leu Val Asp Leu Ser Ala Phe Leu Val Ser Ser Asp

50 55 60

Leu Thr Tyr Val Tyr Gln Trp Pro Trp Thr Leu Leu Leu Leu Ala Val

65 70 75 80

Ser Gly Phe Cys Asn Phe Ala Gln Asn Val Ile Ala Phe Ser Ile Leu

85 90 95

Asn Leu Val Ser Pro Leu Ser Tyr Ser Val Ala Asn Ala Thr Lys Arg

100 105 110

Ile Met Val Ile Thr Val Ser Leu Ile Met Leu Arg Asn Pro Val Thr

115 120 125

Ser Thr Ile Val Leu Gly Met Met Thr Ala Ile Leu Gly Val Phe Leu

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Tyr Asn Lys Thr Lys Tyr Asp Ala Asn Gln Gln Ala Arg Lys His Leu

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Leu Pro Val Thr Thr Ala Asp Leu Ser Ser Lys Glu Arg His Arg Ser

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Pro Leu Glu Lys Pro His Asn Gly Leu Leu Phe Pro Gln His Gly Asp

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Tyr Gln Tyr Gly Arg Asn Asn Ile Leu Thr Asp His Phe Gln Tyr Ser

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gccccctggc tcggcggccc tc atg ccc gcc cta cgt cca ctc ctg ccg ctc 352

Met Pro Ala Leu Arg Pro Leu Leu Pro Leu

1 5 10

ctg ctc ctc ctc cgg ctg acc tcg ggg gct ggc ttg ctg cca ggg ctg 400

Leu Leu Leu Leu Arg Leu Thr Ser Gly Ala Gly Leu Leu Pro Gly Leu

15 20 25

ggg agc cac ccg ggc gtg tgc ccc aac cag ctc agc ccc aac ctg tgg 448

Gly Ser His Pro Gly Val Cys Pro Asn Gln Leu Ser Pro Asn Leu Trp

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gtg gac gcc cag agc acc tgt gag cgc gag tgt agc agg gac cag gac 496

Val Asp Ala Gln Ser Thr Cys Glu Arg Glu Cys Ser Arg Asp Gln Asp

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Cys Ala Ala Ala Glu Lys Cys Cys Ile Asn Val Cys Gly Leu His Ser

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Cys Val Ala Ala Arg Phe Pro Gly Ser Pro Ala Ala Pro Thr Thr Ala
75 80 85 90

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Ala Ser Cys Glu Gly Phe Val Cys Pro Gln Gln Gly Ser Asp Cys Asp
95 100 105

atc tgg gac ggg cag ccc gtg tgc cgc tgc cgc gac cgc tgt gag aag 688
Ile Trp Asp Gly Gln Pro Val Cys Arg Cys Arg Asp Arg Cys Glu Lys
110 115 120

gag ccc agc ttc acc tgc gcc tcg gac ggc ctc acc tac tac aac cgc 736
Glu Pro Ser Phe Thr Cys Ala Ser Asp Gly Leu Thr Tyr Tyr Asn Arg
125 130 135

tgc tat atg gac gcc gag gcc tgc tgc ggg gcc tgc acc tcc aca tcg 784
Cys Tyr Met Asp Ala Glu Ala Cys Cys Gly Ala Cys Thr Ser Thr Ser
140 145 150

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Cys Pro Ala Ser Thr Cys Ser Ala Gly Arg Pro Ala Ala Arg Gly Arg
155 160 165 170

cgg aga cca ctg ccc gcc cca cac ctg ggg ccg cgc ccg tgc ctc ctg 880
Arg Arg Pro Leu Pro Ala Pro His Leu Gly Pro Arg Pro Cys Leu Leu
175 180 185

ccc tgt aca gca gcc cct ccc cac agg cgg tgc agg ttg ggg gta cgg 928

Pro Cys Thr Ala Ala Pro Pro His Arg Arg Cys Arg Leu Gly Val Arg

190

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cca gcc tcc act gcg acg tca gcg gcc gcc cgc cgc ctg ctg 970

Pro Ala Ser Thr Ala Thr Ser Ala Ala Ala Arg Arg Leu Leu

205

210

215

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<212> PRT

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Cys Pro Asn Gln Leu Ser Pro Asn Leu Trp Val Asp Ala Gln Ser Thr

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Cys Glu Arg Glu Cys Ser Arg Asp Gln Asp Cys Ala Ala Ala Glu Lys

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Cys Cys Ile Asn Val Cys Gly Leu His Ser Cys Val Ala Ala Arg Phe

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Pro Gly Ser Pro Ala Ala Pro Thr Thr Ala Ala Ser Cys Glu Gly Phe

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Val Cys Pro Gln Gln Gly Ser Asp Cys Asp Ile Trp Asp Gly Gln Pro

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Val Cys Arg Cys Arg Asp Arg Cys Glu Lys Glu Pro Ser Phe Thr Cys

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Ala Ser Asp Gly Leu Thr Tyr Tyr Asn Arg Cys Tyr Met Asp Ala Glu

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Ala Cys Cys Gly Ala Cys Thr Ser Thr Ser Cys Pro Ala Ser Thr Cys

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Ser Ala Gly Arg Pro Ala Ala Arg Gly Arg Arg Arg Pro Leu Pro Ala

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Pro His Leu Gly Pro Arg Pro Cys Leu Leu Pro Cys Thr Ala Ala Pro

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Ser Ala Ala Ala Arg Arg Leu Leu

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Leu Gln Val Phe Phe Leu Val Phe Pro Asp Gly Val Arg Pro Gln Pro

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Ser Ser Ser Pro Ser Glu Ala Val Pro Thr Ser Leu Glu Leu Gln Arg

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Arg Pro Ala Val Pro Gly Leu Pro Thr Val Val Pro Thr Leu Val Thr

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Pro Ser Ala Pro Gly Asn Arg Thr Val Asp Leu Phe Pro Val Leu Pro

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Ile Cys Val Cys Asp Leu Thr Pro Gly Ala Cys Asp Ile Asn Cys Cys

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Ser Val Ile Phe Arg Ser Asn Ser Pro Phe Pro Ser Arg Val Phe Met

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170

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gcc ctg gct gca gag ttt gga ggc gaa tca ttc act tca aca ttc caa 629

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Thr Gln Ser Pro Pro Ser Phe Tyr Arg Ala Gly Asp Pro Ile Leu Thr

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Tyr Phe Pro Lys Trp Ser Val Ile Ser Leu Leu Arg Gln Pro Ala Gly

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225

230

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Val Gly Ala Gly Gly Thr Leu Cys

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<212> PRT

<213> Homo sapiens

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20 25 30

Pro Thr Ser Leu Glu Leu Gln Arg Gly Thr Asp Gly Gly Thr Leu Gln
35 40 45

Ser Pro Ser Glu Ala Thr Ala Thr Arg Pro Ala Val Pro Gly Leu Pro
50 55 60

Thr Val Val Pro Thr Leu Val Thr Pro Ser Ala Pro Gly Asn Arg Thr
65 70 75 80

Val Asp Leu Phe Pro Val Leu Pro Ile Cys Val Cys Asp Leu Thr Pro
85 90 95

Gly Ala Cys Asp Ile Asn Cys Cys Cys Asp Arg Asp Cys Tyr Leu Leu
100 105 110

His Pro Arg Thr Val Phe Ser Phe Cys Leu Pro Gly Ser Val Arg Ser
115 120 125

Ser Ser Trp Val Cys Val Asp Asn Ser Val Ile Phe Arg Ser Asn Ser
130 135 140

Pro Phe Pro Ser Arg Val Phe Met Asp Ser Asn Gly Ile Arg Gln Phe
145 150 155 160

Cys Val His Val Asn Asn Ser Asn Leu Asn Tyr Phe Gln Lys Leu Gln

165

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175

Lys Val Asn Ala Thr Asn Phe Gln Ala Leu Ala Ala Glu Phe Gly Gly

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185

190

Glu Ser Phe Thr Ser Thr Phe Gln Thr Gln Ser Pro Pro Ser Phe Tyr

195

200

205

Arg Ala Gly Asp Pro Ile Leu Thr Tyr Phe Pro Lys Trp Ser Val Ile

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Ser Leu Leu Arg Gln Pro Ala Gly Val Gly Ala Gly Gly Thr Leu Cys

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Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr

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tcg gtg ccg cga ctt tca cga tgg ctc gcc caa cct tac tac ctt ctg 99

Ser Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu

15

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25

tcg gcc ctg ctc tct gct gcc ttc cta ctc gtg agg aaa ctg ccg ccg 147

Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro

30

35

40

ctc tgc cac ggt ctg ccc acc caa cgc gaa gac ggt aac ccg tgt gac 195

Leu Cys His Gly Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp

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55

60

ttt gac tgg aga gaa gtg gag atc ctg atg ttt ctc agt gcc att gtg 243

Phe Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val

65

70

75

atg atg aag aac cgc aga tcc atc act gtg gag caa cat ata ggc aac 291

Met Met Lys Asn Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn

80

85

90

att ttc atg ttt agt aaa gtg gcc aac aca att ctt ttc ttc cgc ttg 339

Ile Phe Met Phe Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu

95

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105

gat att cgc atg ggc cta ctt tac atc aca ctc tgc ata gtg ttc ctg 387

Asp Ile Arg Met Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu

110

115

120

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Met Thr Cys Lys Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr
125 130 135 140

ttc aat gat aaa acc att gat gag gaa cta gaa cgg gac aag agg gtc 483
Phe Asn Asp Lys Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val
145 150 155

act tgg att gtg gag ttc ttt gcc aat tgg tct aat gac tgc caa tca 531
Thr Trp Ile Val Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser
160 165 170

ttt gcc cct atc tat gct gac ctc tcc ctt aaa tac aac tgt aca ggg 579
Phe Ala Pro Ile Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly
175 180 185

cta aat ttt ggg aag gtg gat gtt gga cgc tat act gat gtt agt acg 627
Leu Asn Phe Gly Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr
190 195 200

cgg tac aaa gtg agc aca tca ccc ctc acc aag caa ctc cct acc ctg 675
Arg Tyr Lys Val Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu
205 210 215 220

atc ctg ttc caa ggt ggc aag gag gca atg cgg cgg cca cag att gac 723
Ile Leu Phe Gln Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp
225 230 235

aag aaa gga cgg gct gtc tca tgg acc ttc tct gag gag aat gtg atc 771

Lys Lys Gly Arg Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile

240

245

250

cga gaa ttt aac tta aat gag cta tac cag cgg gcc aag aaa cta tca 819

Arg Glu Phe Asn Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser

255

260

265

aag gct gga gac aat atc cct gag gag cag cct gtg gct caa ccc cca 867

Lys Ala Gly Asp Asn Ile Pro Glu Glu Gln Pro Val Ala Gln Pro Pro

270

275

280

cca cag tgt cag atg ggg aaa aca aga agg ata aat aag atc ctc act 915

Pro Gln Cys Gln Met Gly Lys Thr Arg Arg Ile Asn Lys Ile Leu Thr

285

290

295

300

ttg gca gtg ctg cct ctc ctg tca att cca ggc tct ttc cat aac cac 963

Leu Ala Val Leu Pro Leu Leu Ser Ile Pro Gly Ser Phe His Asn His

305

310

315

~~aag cct gag gct gca gcc ttt tat tta tgt ttt ccc ttt ggc tgt gac 1011~~

Lys Pro Glu Ala Ala Ala Phe Tyr Leu Cys Phe Pro Phe Gly Cys Asp

320

325

330

tgg gtg ggg cag cat gca gct tct gat ttt aaa gag gca tct agg gaa 1059

Trp Val Gly Gln His Ala Ala Ser Asp Phe Lys Glu Ala Ser Arg Glu

335

340

345

ttg tca ggc acc cta cag gaa ggc ctg cca tgc tgt ggc caa ctg ttt 1107

Leu Ser Gly Thr Leu Gln Glu Gly Leu Pro Cys Cys Gly Gln Leu Phe

350

355

360

cac tgg agc aag aaa gag atc tca taggacggag ggggaaatgg tttccctcca 1161

His Trp Ser Lys Lys Glu Ile Ser

365

370

agcttgggtc agtgtgttaa ctgcttatca gctattcaga catctccatg gtttctccat 1221

gaaactctgt ggtttcatca ttccttctta gttgacctgc acagcttggt tagacctaga 1281

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1631

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<212> PRT

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<400> 38

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Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly

35 40 45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg

50 55 60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn

65 70 75 80

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe

85 90 95

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met

100 105 110

Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys

115 120 125

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys

130 135 140

Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val

145 150 155 160

Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile

165 170 175

Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly

180 185 190

Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val

195 200 205

Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln

210 215 220

Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg

225 230 235 240

Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn

245 250 255

Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp

260 265 270

Asn Ile Pro Glu Glu Gln Pro Val Ala Gln Pro Pro Pro Gln Cys Gln

275 280 285

Met Gly Lys Thr Arg Arg Ile Asn Lys Ile Leu Thr Leu Ala Val Leu

290 295 300

Pro Leu Leu Ser Ile Pro Gly Ser Phe His Asn His Lys Pro Glu Ala
305 310 315 320

Ala Ala Phe Tyr Leu Cys Phe Pro Phe Gly Cys Asp Trp Val Gly Gln
325 330 335

His Ala Ala Ser Asp Phe Lys Glu Ala Ser Arg Glu Leu Ser Gly Thr
340 345 350

Leu Gln Glu Gly Leu Pro Cys Cys Gly Gln Leu Phe His Trp Ser Lys
355 360 365

Lys Glu Ile Ser
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<222> (122)..(1270)

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c atg gca ggg att cca ggg ctc ctc ttc ctt ctc ttc ttt ctg ctc tgt 169

Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu Cys

1 5 10 15

gct gtt ggg caa gtg agc cct tac agt gcc ccc tgg aaa ccc act tgg 217

Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr Trp

20 25 30

cct gca tac cgc ctc cct gtc gtc ttg ccc cag tct acc ctc aat tta 265

Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu

35 40 45

gcc-aag-cca-gac ttt gga-gcc gaa gcc aaa tta gaa-gta tct tct tca 313

Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser Ser

50 55 60

tgt gga ccc cag tgt cat aag gga act cca ctg ccc act tac gaa gag 361

Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Glu Glu

65 70 75 80

gcc aag caa tat ctg tct tat gaa acg ctc tat gcc aat ggc agc cgc 409

Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg

85 90 95

aca gag acg cag gtg ggc atc tac atc ctc agc agt agt gga gat ggg 457

Thr Glu Thr Gln Val Gly Ile Tyr Ile Leu Ser Ser Ser Gly Asp Gly

100 105 110

gcc caa cac cga gac tca ggg tct tca gga aag tct cga agg aag cgg 505

Ala Gln His Arg Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys Arg

115

120

125

cag att tat ggc tat gac agc agg ttc agc att ttt ggg aag gac ttc 553

Gln Ile Tyr Gly Tyr Asp Ser Arg Phe Ser Ile Phe Gly Lys Asp Phe

130

135

140

ctg ctc aac tac cct ttc tca aca tca gtg aag tta tcc acg ggc tgc 601

Leu Leu Asn Tyr Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly Cys

145

150

155

160

acc ggc acc ctg gtg gca gag aag cat gtc ctc aca gct gcc cac tgc 649

Thr Gly Thr Leu Val Ala Glu Lys His Val Leu Thr Ala Ala His Cys

165

170

175

ata cac gat gga aaa acc tat gtg aaa gga acc cag aag ctt cga gtg 697

Ile His Asp Gly Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val

180

185

190

ggc ttc cta aag ccc aag ttt aaa gat ggt ggt cga ggg gcc aac gac 745

Gly Phe Leu Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp

195

200

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tcc act tca gcc atg ccc gag cag atg aaa ttt cag tgg atc cgg gtg 793

Ser Thr Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val

210

215

220

aaa cgc acc cat gtg ccc aag ggt tgg atc aag ggc aat gcc aat gac 841

Lys Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp
225 230 235 240

atc ggc atg gat tat gat tat gcc ctc ctg gaa ctc aaa aag ccc cac 889
Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His
245 250 255

aag aga aaa ttt atg aag att ggg gtg agc cct cct gct aag cag ctg 937
Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu
260 265 270

cca ggg gac aga att cac ttc tct ggt tat gac aat gac cga cca ggc 985
Pro Gly Asp Arg Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly
275 280 285

aat ttg gtg tat cgc ttc tgt gac gtc aaa gac gag acc tat gac ttg 1033
Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu
290 295 300

ctc tac cag caa tgc gat gcc cag cca ggg gcc agc ggg tct ggg gtc 1081
Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala Ser Gly Ser Gly Val

305 310 315 320

tat gtg agg atg tgg aag aga cag cag cag aag tgg gag cga aaa att 1129
Tyr Val Arg Met Trp Lys Arg Gln Gln Gln Lys Trp Glu Arg Lys Ile
325 330 335

att ggc att ttt tca ggg cac cag tgg gtg gac atg aat ggt tcc cca 1177
Ile Gly Ile Phe Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro

340

345

350

cag gat ttc aac gtg gct gtc aga atc act cct ctc aaa tat gcc cag 1225

Gln Asp Phe Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln

355

360

365

att tgc tat tgg att aaa gga aac tac ctg gat tgt agg gag ggg 1270

Ile Cys Tyr Trp Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly

370

375

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<211> 383

<212> PRT

<213> Homo sapiens

<400> 40

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Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu

35 40 45

Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser Ser

50 55 60

Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Glu Glu

65 70 75 80

Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg

85 90 95

Thr Glu Thr Gln Val Gly Ile Tyr Ile Leu Ser Ser Ser Gly Asp Gly

100

105

110

Ala Gln His Arg Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys Arg

115

120

125

Gln Ile Tyr Gly Tyr Asp Ser Arg Phe Ser Ile Phe Gly Lys Asp Phe

130

135

140

Leu Leu Asn Tyr Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly Cys

145

150

155

160

Thr Gly Thr Leu Val Ala Glu Lys His Val Leu Thr Ala Ala His Cys

165

170

175

Ile His Asp Gly Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val

180

185

190

Gly Phe Leu Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp

195

200

205

Ser Thr Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val

210

215

220

Lys Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp

225

230

235

240

Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His

245

250

255

Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu

260

265

270

Pro Gly Asp Arg Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly

275

280

285

Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu

290

295

300

Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala Ser Gly Ser Gly Val

305

310

315

320

Tyr Val Arg Met Trp Lys Arg Gln Gln Gln Lys Trp Glu Arg Lys Ile

325

330

335

Ile Gly Ile Phe Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro

340

345

350

Gln Asp Phe Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln

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360

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Ile Cys Tyr Trp Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly

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Gly Ile Lys Ala Leu Ile Ser Leu Ser Phe Gly Gly Ala Ile Gly Leu

5

10

15

atg ttt ttg atg ctt gga tgt gcc ctt cca ata tac aac aaa tac tgg 153

Met Phe Leu Met Leu Gly Cys Ala Leu Pro Ile Tyr Asn Lys Tyr Trp

20

25

30

ccc ctc ttt gtt cta ttt ttt tac atc ctt tca cct att cca tac tgc 201

Pro Leu Phe Val Leu Phe Phe Tyr Ile Leu Ser Pro Ile Pro Tyr Cys

35

40

45

50

ata gca aga aga tta gtg gat gat aca gat gct atg agt aac gct tgt 249

Ile Ala Arg Arg Leu Val Asp Asp Thr Asp Ala Met Ser Asn Ala Cys

55

60

65

aag gaa ctt gcc atc ttt ctt aca acg ggc att gtc gtg tca gct ttt 297

Lys Glu Leu Ala Ile Phe Leu Thr Thr Gly Ile Val Val Ser Ala Phe

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75

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gga ctc cct att gta ttt gcc aga gca cat ctg att gag tgg gga gct 345

Gly Leu Pro Ile Val Phe Ala Arg Ala His Leu Ile Glu Trp Gly Ala

85

90

95

tgt gca ctt gtt ctc aca gga aac aca gtc atc ttt gca act ata cta 393

Cys Ala Leu Val Leu Thr Gly Asn Thr Val Ile Phe Ala Thr Ile Leu

100

105

110

ggc ttt ttc ttg gtc ttt gga agc aat gac gac ttc agc tgg cag cag 441

Gly Phe Phe Leu Val Phe Gly Ser Asn Asp Asp Phe Ser Trp Gln Gln

115

120

125

130

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gggtatttta ggtgctccct tctcactttt attgtaagca tactattttc acagagactt 614

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<213> Homo sapiens

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Tyr Trp Pro Leu Phe Val Leu Phe Phe Tyr Ile Leu Ser Pro Ile Pro

35 40 45

Tyr Cys Ile Ala Arg Arg Leu Val Asp Asp Thr Asp Ala Met Ser Asn

50 55 60

Ala Cys Lys Glu Leu Ala Ile Phe Leu Thr Thr Gly Ile Val Val Ser

65 70 75 80

Ala Phe Gly Leu Pro Ile Val Phe Ala Arg Ala His Leu Ile Glu Trp

85 90 95

Gly Ala Cys Ala Leu Val Leu Thr Gly Asn Thr Val Ile Phe Ala Thr

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Met Pro Pro Pro

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Val Ser Ser Ala Val Ile Leu Thr Lys Ala Val Gly Gly Asn Glu Ala

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gct gca ata ttt aat tca gcc ttt gga agt ttt ttg ggc atc gtt ata 213

Ala Ala Ile Phe Asn Ser Ala Phe Gly Ser Phe Leu Gly Ile Val Ile

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Thr Pro Leu Leu Leu Leu Phe Leu Gly Ser Ser Ser Ser Val Pro

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ttc aca tct att ttt tct cag ctt ttt atg act gtt gtg gtt cct ctc 309

Phe Thr Ser Ile Phe Ser Gln Leu Phe Met Thr Val Val Val Pro Leu

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atc att gga cag att gtc cga aga tac atc aag gat tgg ctt gag aga 357

~~Ile Ile Gly Gln Ile Val Arg Arg Tyr Ile Lys Asp Trp Leu Glu Arg~~

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Ile Tyr Thr Thr Phe Cys Asp Thr Phe Ser Asn Pro Asn Ile Asp Leu

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gat aaa ttc agc ctt gtt ctc ata ctg ttc ata ata ttt tct atc cag 501

Asp Lys Phe Ser Leu Val Leu Ile Leu Phe Ile Ile Phe Ser Ile Gln

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Gly Phe Thr Pro Ala Asp Thr Val Ala Ile Ile Phe Cys Ser Thr His

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aaa tcc ctt aca ttg gga att ccg atg ctg aag atc gtg ttt gca ggc 645

Lys Ser Leu Thr Leu Gly Ile Pro Met Leu Lys Ile Val Phe Ala Gly

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cat gag tat ctc tct tta ata tct gta ccc ttg ctc atc tac cac cca 693

His Glu Tyr Leu Ser Leu Ile Ser Val Pro Leu Leu Ile Tyr His Pro

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gct cag atc ctt ctg gga agt gtg ttg gtg cca aca atc aag tct tgg 741

Ala Gln Ile Leu Leu Gly Ser Val Leu Val Pro Thr Ile Lys Ser Trp

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atg gta tca agg cag aag gga gtg aag ctg aca agg ccg aca gta 786

Met Val Ser Arg Gln Lys Gly Val Lys Leu Thr Arg Pro Thr Val

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30

Gly Ile Val Ile Thr Pro Leu Leu Leu Leu Phe Leu Gly Ser Ser

35

40

45

Ser Ser Val Pro Phe Thr Ser Ile Phe Ser Gln Leu Phe Met Thr Val

50

55

60

Val Val Pro Leu Ile Ile Gly Gln Ile Val Arg Arg Tyr Ile Lys Asp

65

70

75

80

Trp-Leu Glu Arg-Lys Lys Pro Pro Phe Gly Ala Ile Ser Ser Ser Val

85

90

95

Leu Leu Met Ile Ile Tyr Thr Thr Phe Cys Asp Thr Phe Ser Asn Pro

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105

110

Asn Ile Asp Leu Asp Lys Phe Ser Leu Val Leu Ile Leu Phe Ile Ile

115

120

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Phe Ser Ile Gln Leu Ser Phe Met Leu Leu Thr Phe Ile Phe Ser Thr

130

135

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Arg Asn Asn Ser Gly Phe Thr Pro Ala Asp Thr Val Ala Ile Ile Phe

145

150

155

160

Cys Ser Thr His Lys Ser Leu Thr Leu Gly Ile Pro Met Leu Lys Ile

165

170

175

Val Phe Ala Gly His Glu Tyr Leu Ser Leu Ile Ser Val Pro Leu Leu

180

185

190

Ile Tyr His Pro Ala Gln Ile Leu Leu Gly Ser Val Leu Val Pro Thr

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Ile Lys Ser Trp Met Val Ser Arg Gln Lys Gly Val Lys Leu Thr Arg

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Pro Thr Val

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gcacggcctc taggtctcct cgccaggaca gcaacctctc ccctggccct c atg ggc 297

Met Gly

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acc gtc agc tcc agg cgg tcc tgg tgg ccg ctg cca ctg ctg ctg ctg 345

Thr Val Ser Ser Arg Arg Ser Trp Trp Pro Leu Pro Leu Leu Leu Leu

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15

ctg ctg ctg ctc ctg ggt ccc gcg ggc gcc cgt gcg cag gag gac gag 393

Leu Leu Leu Leu Leu Gly Pro Ala Gly Ala Arg Ala Gln Glu Asp Glu

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25

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gac ggc gac tac gag gag ctg gtg cta gcc ttg cgt tcc gag gag gac 441

Asp Gly Asp Tyr Glu Glu Leu Val Leu Ala Leu Arg Ser Glu Glu Asp

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ggc ctg gcc gaa gca ccc gag cac gga acc aca gcc acc ttc cac cgc 489

Gly Leu Ala Glu Ala Pro Glu His Gly Thr Thr Ala Thr Phe His Arg

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tgc gcc aag gat ccg tgg agg ttg cct ggc acc tac gtg gtg gtg ctg 537

Cys Ala Lys Asp Pro Trp Arg Leu Pro Gly Thr Tyr Val Val Val Leu

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aag gag gag acc cac ctc tcg cag tca gag cgc act gcc cgc cgc ctg 585

Lys Glu Glu Thr His Leu Ser Gln Ser Glu Arg Thr Ala Arg Arg Leu

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90

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cag gcc cag gct gcc cgc cgg gga tac ctc acc aag atc ctg cat gtc 633

Gln Ala Gln Ala Ala Arg Arg Gly Tyr Leu Thr Lys Ile Leu His Val

100

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ttc cat ggc ctt ctt cct ggc ttc ctg gtg aag atg agt ggc gac ctg 681

Phe His Gly Leu Leu Pro Gly Phe Leu Val Lys Met Ser Gly Asp Leu

115

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ctg gag ctg gcc ttg aag ttg ccc cat gtc gac tac atc gag gag gac 729

Leu Glu Leu Ala Leu Lys Leu Pro His Val Asp Tyr Ile Glu Glu Asp

135

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145

tcc tct gtc ttt gcc cag agc atc ccg tgg aac ctg gag cgg att acc 777

Ser Ser Val Phe Ala Gln Ser Ile Pro Trp Asn Leu Glu Arg Ile Thr

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cct cca cgg tac cgg gcg gat gaa tac cag ccc ccc gac gga ggc agc 825

Pro Pro Arg Tyr Arg Ala Asp Glu Tyr Gln Pro Pro Asp Gly Gly Ser

165

170

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ctg gtg gag gtg tat ctc cta gac acc agc ata cag agt gac cac cgg 873

Leu Val Glu Val Tyr Leu Leu Asp Thr Ser Ile Gln Ser Asp His Arg

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gaa atc gag ggc agg gtc atg gtc acc gac ttc gag aat gtg ccc gag 921

Glu Ile Glu Gly Arg Val Met Val Thr Asp Phe Glu Asn Val Pro Glu

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Glu Asp Gly Thr Arg Phe His Arg Gln Ala Ser Lys Cys Asp Ser His				
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ggc acc cac ctg gca ggg gtg gtc agc ggc cgg gat gcc ggc gtg gcc				1017
Gly Thr His Leu Ala Gly Val Val Ser Gly Arg Asp Ala Gly Val Ala				
	230	235	240	
aag ggt gcc agc atg cgc agc ctg cgc gtg ctc aac tgc caa ggg aag				1065
Lys Gly Ala Ser Met Arg Ser Leu Arg Val Leu Asn Cys Gln Gly Lys				
	245	250	255	
ggc acg gtt agc ggc acc ctc ata ggc ctg gag ttt att cgg aaa agc				1113
Gly Thr Val Ser Gly Thr Leu Ile Gly Leu Glu Phe Ile Arg Lys Ser				
	260	265	270	
cag ctg gtc cag cct gtg ggg cca ctg gtg gtg ctg ctg ccc ctg gcg				1161
Gln Leu Val Gln Pro Val Gly Pro Leu Val Val Leu Leu Pro Leu Ala				
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ggg ggt tac agc cgc gtc ctc aac gcc gcc tgc cag cgc ctg gcg agg				1209
Gly Gly Tyr Ser Arg Val Leu Asn Ala Ala Cys Gln Arg Leu Ala Arg				
	295	300	305	
gct ggg gtc gtg ctg gtc acc gct gcc ggc aac ttc cgg gac gat gcc				1257
Ala Gly Val Val Leu Val Thr Ala Ala Gly Asn Phe Arg Asp Asp Ala				
	310	315	320	

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Cys Leu Tyr Ser Pro Ala Ser Ala Pro Glu Val Ile Thr Val Gly Ala

325

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acc aat gcc cag gac cag ccg gtg acc ctg ggg act ttg ggg acc aac 1353

Thr Asn Ala Gln Asp Gln Pro Val Thr Leu Gly Thr Leu Gly Thr Asn

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360

365

370

gcc tcc agc gac tgc agc acc tgc ttt gtg tca cag agt ggg aca tca 1449

Ala Ser Ser Asp Cys Ser Thr Cys Phe Val Ser Gln Ser Gly Thr Ser

375

380

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cag gct gct gcc cac gtg gct ggc att gca gcc atg atg ctg tct gcc 1497

Gln Ala Ala Ala His Val Ala Gly Ile Ala Ala Met Met Leu Ser Ala

390

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Glu Pro Glu Leu Thr Leu Ala Glu Leu Arg Gln Arg Leu Ile His Phe

405

410

415

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Ser Ala Lys Asp Ala Ile Asn Glu Ala Trp Phe Pro Glu Asp Gln Arg

420

425

430

gta ctg acc ccc aac ctg gtg gcc gcc ctg ccc ccc agc acc cat ggg 1641

Val Leu Thr Pro Asn Leu Val Ala Ala Leu Pro Pro Ser Thr His Gly

435 440 445 450

gca ggt tgg cag ctg ttt tgc agg act gtg tgg tca gca cac tcg ggg 1689

Ala Gly Trp Gln Leu Phe Cys Arg Thr Val Trp Ser Ala His Ser Gly

455 460 465

cct aca cgg atg gcc aca gcc atc gcc cgc tgc gcc cca gat gag gag 1737

Pro Thr Arg Met Ala Thr Ala Ile Ala Arg Cys Ala Pro Asp Glu Glu

470 475 480

ctg ctg agc tgc tcc agt ttc tcc agg agt gga agc ggc ggg gcg agc 1785

Leu Leu Ser Cys Ser Ser Phe Ser Arg Ser Gly Ser Gly Gly Ala Ser

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Ala Trp Arg Pro Lys Gly Ala Ser Trp Ser Ala Gly Pro Thr Thr Leu

500 505 510

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Leu Gly Val Arg Val Ser Thr Pro Leu Pro Gly Ala Ala Cys Tyr Pro

515 520 525 530

agg cca act gca gcg tcc aca cag ctc cac cag ctg agg cca gca tgg 1929

Arg Pro Thr Ala Ala Ser Thr Gln Leu His Gln Leu Arg Pro Ala Trp

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Gly Pro Val Ser Thr Ala Thr Asn Arg Ala Thr Ser Ser Gln Ala Ala

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Ala Pro Thr Gly Arg Trp Arg Thr Leu Ala Pro Thr Ser Arg Leu Cys

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Asp Glu Asp Gly Asp Tyr Glu Glu Leu Val Leu Ala Leu Arg Ser Glu

35

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Glu Asp Gly Leu Ala Glu Ala Pro Glu His Gly Thr Thr Ala Thr Phe

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55

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His Arg Cys Ala Lys Asp Pro Trp Arg Leu Pro Gly Thr Tyr Val Val

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Val Leu Lys Glu Glu Thr His Leu Ser Gln Ser Glu Arg Thr Ala Arg

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90

95

Arg Leu Gln Ala Gln Ala Ala Arg Arg Gly Tyr Leu Thr Lys Ile Leu

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105

110

His Val Phe His Gly Leu Leu Pro Gly Phe Leu Val Lys Met Ser Gly

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Asp Leu Leu Glu Leu Ala Leu Lys Leu Pro His Val Asp Tyr Ile Glu

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Glu Asp Ser Ser Val Phe Ala Gln Ser Ile Pro Trp Asn Leu Glu Arg

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Ile Thr Pro Pro Arg Tyr Arg Ala Asp Glu Tyr Gln Pro Pro Asp Gly

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Gly Ser Leu Val Glu Val Tyr Leu Leu Asp Thr Ser Ile Gln Ser Asp

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His Arg Glu Ile Glu Gly Arg Val Met Val Thr Asp Phe Glu Asn Val

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Pro Glu Glu Asp Gly Thr Arg Phe His Arg Gln Ala Ser Lys Cys Asp

210

215

220

Ser His Gly Thr His Leu Ala Gly Val Val Ser Gly Arg Asp Ala Gly

225

230

235

240

Val Ala Lys Gly Ala Ser Met Arg Ser Leu Arg Val Leu Asn Cys Gln

245

250

255

Gly Lys Gly Thr Val Ser Gly Thr Leu Ile Gly Leu Glu Phe Ile Arg

260

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Lys Ser Gln Leu Val Gln Pro Val Gly Pro Leu Val Val Leu Leu Pro

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Ala Arg Ala Gly Val Val Leu Val Thr Ala Ala Gly Asn Phe Arg Asp

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Asp Ala Cys Leu Tyr Ser Pro Ala Ser Ala Pro Glu Val Ile Thr Val

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Gly Ala Thr Asn Ala Gln Asp Gln Pro Val Thr Leu Gly Thr Leu Gly

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Ile Gly Ala Ser Ser Asp Cys Ser Thr Cys Phe Val Ser Gln Ser Gly

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Thr Ser Gln Ala Ala Ala His Val Ala Gly Ile Ala Ala Met Met Leu

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Ser Ala Glu Pro Glu Leu Thr Leu Ala Glu Leu Arg Gln Arg Leu Ile

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His Phe Ser Ala Lys Asp Ala Ile Asn Glu Ala Trp Phe Pro Glu Asp

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Gln Arg Val Leu Thr Pro Asn Leu Val Ala Ala Leu Pro Pro Ser Thr

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His Gly Ala Gly Trp Gln Leu Phe Cys Arg Thr Val Trp Ser Ala His

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Ser Gly Pro Thr Arg Met Ala Thr Ala Ile Ala Arg Cys Ala Pro Asp

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Glu Glu Leu Leu Ser Cys Ser Ser Phe Ser Arg Ser Gly Ser Gly Gly

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Ala Ser Ala Trp Arg Pro Lys Gly Ala Ser Trp Ser Ala Gly Pro Thr

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Ala Trp Gly Pro Val Ser Thr Ala Thr Asn Arg Ala Thr Ser Ser Gln

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 Thr Gly Ala Leu Arg Ala Ser Leu Val His Val Gly Ser Arg Pro Tyr
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 Thr Glu Phe Pro Phe Gly Gln His Ser Ser Gly Glu Ala Ala Gln Asp
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 Ala Leu Val Tyr Ala Lys Glu Gln Leu Phe Ala Glu Ala Ser Gly Ala
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 Arg Pro Gly Val Pro Lys Val Leu Val Trp Val Thr Asp Gly Gly Ser
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Gly His Gly Leu Arg Arg Gly Ala Ser Ala

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Gly Asp Leu Met Phe Leu Leu Asp Ser Ser Ala Ser Val Ser His Tyr

35 40 45

Glu Phe Ser Arg Val Arg Glu Phe Val Gly Gln Leu Val Ala Pro Leu

50 55 60

Pro Leu Gly Thr Gly Ala Leu Arg Ala Ser Leu Val His Val Gly Ser

65 70 75 80

Arg Pro Tyr Thr Glu Phe Pro Phe Gly Gln His Ser Ser Gly Glu Ala

85 90 95

Ala Gln Asp Ala Val Arg Ala Ser Ala Gln Arg Met Gly Asp Thr His

100 105 110

Thr Gly Leu Ala Leu Val Tyr Ala Lys Glu Gln Leu Phe Ala Glu Ala

115 120 125

Ser Gly Ala Arg Pro Gly Val Pro Lys Val Leu Val Trp Val Thr Asp

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Gly Gly Ser Ser Asp Pro Val Gly Pro Pro Met Gln Glu Leu Lys Asp

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Leu Gly Val Thr Val Phe Ile Val Ser Thr Gly Arg Gly Asn Phe Leu

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Glu Leu Ser Ala Ala Ala Ser Ala Pro Ala Glu Lys His Leu His Phe

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Val Asp Val Asp Asp Leu His Ile Ile Val Gln Glu Leu Arg Gly Ser

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200

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Ile Leu Asp Ala Met Arg Pro Gln Gln Leu His Ala Thr Glu Ile Thr

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Ser Ser Gly Phe Arg Leu Ala Trp Pro Pro Leu Leu Thr Ala Asp Ser

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Gly Tyr Tyr Val Leu Gly Leu Val Pro Ser Ala Gln Pro Gly Gly Cys

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Cys Gly Asn Ile Val Thr Phe Ala Gln Phe Leu Phe Ile Ala Val Glu

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Gly Phe Leu Phe Glu Ala Asp Leu Gly Arg Lys Pro Pro Ala Ile Pro

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Val Ser Val Gly Ile Phe Ile Cys Thr Phe Met Ser Ala Lys Gln Val

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Thr Ser Gln Ser Ser Leu Ser Glu Asn Asp Gly Phe Gln Ala Phe Val

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Trp Trp Leu Leu Gly Ile Gly Ala Leu Thr Phe Ala Leu Leu Met Ser

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Ala Arg Met Gly Ile Phe Gln Glu Thr Leu Tyr Lys Arg Phe Gly Lys

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His Ser Lys Glu Ala Leu Phe Tyr Asn His Ala Leu Pro Leu Pro Gly

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Phe Val Phe Leu Ala Ser Asp Ile Tyr Asp His Ala Val Leu Phe Asn

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aag tct gag tta tat gaa att ccc gtc atc gga gtg acc ctg ccc atc 843

Lys Ser Glu Leu Tyr Glu Ile Pro Val Ile Gly Val Thr Leu Pro Ile

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Met Trp Phe Tyr Leu Leu Met Asn Ile Ile Thr Gln Tyr Val Cys Ile

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cgg ggt gtg ttt atc ctc acc aca gaa tgc gcc tcc ctc acc gtc acg 939

Arg Gly Val Phe Ile Leu Thr Thr Glu Cys Ala Ser Leu Thr Val Thr

255 260 265 270

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Leu Val Val Thr Leu Arg Lys Phe Val Ser Leu Ile Phe Ser Ile Leu

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Tyr Phe Gln Asn Pro Phe Thr Leu Trp His Trp Leu Gly Thr Leu Phe

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Leu Phe Glu Ala Asp Leu Gly Arg Lys Pro Pro Ala Ile Pro Ile Arg

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Tyr Tyr Ala Ile Met Val Thr Met Phe Phe Thr Val Ser Val Val Asn

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Asn Tyr Ala Leu Asn Leu Asn Ile Ala Met Pro Leu His Met Ile Phe

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Arg Ser Gly Ser Leu Ile Ala Asn Met Ile Leu Gly Ile Ile Ile Leu

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Lys Lys Arg Tyr Ser Ile Phe Lys Tyr Thr Ser Ile Ala Leu Val Ser

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Val Gly Ile Phe Ile Cys Thr Phe Met Ser Ala Lys Gln Val Thr Ser

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Gln Ser Ser Leu Ser Glu Asn Asp Gly Phe Gln Ala Phe Val Trp Trp

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160

Leu Leu Gly Ile Gly Ala Leu Thr Phe Ala Leu Leu Met Ser Ala Arg

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170

175

Met Gly Ile Phe Gln Glu Thr Leu Tyr Lys Arg Phe Gly Lys His Ser

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185

190

Lys Glu Ala Leu Phe Tyr Asn His Ala Leu Pro Leu Pro Gly Phe Val

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Phe Tyr Leu Leu Met Asn Ile Ile Thr Gln Tyr Val Cys Ile Arg Gly

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Val Phe Ile Leu Thr Thr Glu Cys Ala Ser Leu Thr Val Thr Leu Val

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Val Thr Leu Arg Lys Phe Val Ser Leu Ile Phe Ser Ile Leu Tyr Phe

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Gln Asn Pro Phe Thr Leu Trp His Trp Leu Gly Thr Leu Phe Val Phe

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Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr Ser Ser

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Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys Gly Leu
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Trp Met Glu Cys Ala Thr His Ser Thr Gly Ile Thr Gln Cys Asp Ile
55 60 65

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Ala Leu Tyr Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly

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Thr Gly Tyr Val

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Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys

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Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly Ile Thr Gln Cys

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Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala Asp Ile Gln Ala Ala

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Gln Ala Met Met Val Thr Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile

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Ile Ser Val Val Gly Met Arg Cys Thr Val Phe Cys Gln Glu Ser Arg

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Ala Lys Asp Arg Val Ala Val Ala Gly Gly Val Phe Phe Ile Leu Gly

115

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Gly Leu Leu Gly Phe Ile Pro Val Ala Trp Asn Leu His Gly Ile Leu

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Arg Asp Phe Tyr Ser Pro Leu Val Pro Asp Ser Met Lys Phe Glu Ile

145

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Gly Glu Ala Leu Tyr Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile

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Ala Gly Ile Ile Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser

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Asn Tyr Tyr Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser

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Leu Leu Ala Leu Cys Leu Leu Leu Pro Leu Leu Leu Leu Gly Gly Trp

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aag cgc tgg cgc cgg ggg cgg gcg gcc cgg cat gta gta gcg gtg gtg 148

Lys Arg Trp Arg Arg Gly Arg Ala Ala Arg His Val Val Ala Val Val

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ctg ggc gac gtg ggc cgc agc ccc cgt atg cag tac cac gcg ctg tcg 196

Leu Gly Asp Val Gly Arg Ser Pro Arg Met Gln Tyr His Ala Leu Ser

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ttg gcc atg cac ggc ttc tcg gtg acc ctc ctg ggg ttc tgc aac tcc 244

Leu Ala Met His Gly Phe Ser Val Thr Leu Leu Gly Phe Cys Asn Ser

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aaa ccc cat gat gag ctc ttg cag aac aac aga att cag att gtg ggg 292

Lys Pro His Asp Glu Leu Leu Gln Asn Asn Arg Ile Gln Ile Val Gly

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ttg aca gaa ctt cag agt ctt gca gtt ggg ccc cgg gtt ttc cag tac 340

Leu Thr Glu Leu Gln Ser Leu Ala Val Gly Pro Arg Val Phe Gln Tyr

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95

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gga gtc aaa gtt gta ctt cag gct atg tac ttg ctg tgg aag ctg atg 388

Gly Val Lys Val Val Leu Gln Ala Met Tyr Leu Leu Trp Lys Leu Met

105

110

115

tgg agg gag cca ggt gcc tat atc ttt ctc cag aac ccc cca ggt ctg 436

Trp Arg Glu Pro Gly Ala Tyr Ile Phe Leu Gln Asn Pro Pro Gly Leu

120

125

130

135

ccg agc att gct gtc tgc tgg ttc gtg ggc tgc ctt tgt gga agc aag 484

Pro Ser Ile Ala Val Cys Trp Phe Val Gly Cys Leu Cys Gly Ser Lys

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145

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ctc gtc att gac tgg cac aac tat ggc tac tcc atc atg ggt ctg gtg 532

Leu Val Ile Asp Trp His Asn Tyr Gly Tyr Ser Ile Met Gly Leu Val

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165

cat ggc ccc aac cat ccc ctc gtt ctg ctg gcc aag tgg tac gag aag 580

His Gly Pro Asn His Pro Leu Val Leu Leu Ala Lys Trp Tyr Glu Lys

170

175

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ttc ttt ggg cgc ctg tcc cac ctg aac ctg tgt gtt acc aat gct atg 628

Phe Phe Gly Arg Leu Ser His Leu Asn Leu Cys Val Thr Asn Ala Met

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190

195

cga gaa gac ctg gcg gat aac tgg cac atc agg gct gtg acc gtc tac 676

Arg Glu Asp Leu Ala Asp Asn Trp His Ile Arg Ala Val Thr Val Tyr

200 205 210 215

gac aag ccc gca tct ttc ttt aaa gag aca cct ctg gac ctg cag cac 724

Asp Lys Pro Ala Ser Phe Phe Lys Glu Thr Pro Leu Asp Leu Gln His

220 225 230

cgg ctc ttc atg aag ctg ggc agc atg cac tct ccg ttc agg gcc cgc 772

Arg Leu Phe Met Lys Leu Gly Ser Met His Ser Pro Phe Arg Ala Arg

235 240 245

tca gaa cct gag gac cca gtc acg gag cgg tcg gcc ttc acg gag cgg 820

Ser Glu Pro Glu Asp Pro Val Thr Glu Arg Ser Ala Phe Thr Glu Arg

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gat gct ggg agc ggg ctg gtg acg cgt ctc cgt gag cgg cca gcc ctg 868

Asp Ala Gly Ser Gly Leu Val Thr Arg Leu Arg Glu Arg Pro Ala Leu

265 270 275

ctg gtc agc agc acg agc tgg aca gag gac gaa gac ttc tcc atc ctg 916

~~Leu Val Ser Ser Thr Ser Trp Thr Glu Asp Glu Asp Phe Ser Ile Leu~~

280 285 290 295

ctg gca gct tta gaa aag ttt gaa caa ctg act ctt gat gga cac aac 964

Leu Ala Ala Leu Glu Lys Phe Glu Gln Leu Thr Leu Asp Gly His Asn

300 305 310

ctt cct tct ctc gtc tgt gtg ata aca ggc aaa ggg cct ctg agg gag 1012

Leu Pro Ser Leu Val Cys Val Ile Thr Gly Lys Gly Pro Leu Arg Glu

315

320

325

tat tat agc cgc ctc atc cac cag aag cac ttc cag cac atc cag gtc 1060

Tyr Tyr Ser Arg Leu Ile His Gln Lys His Phe Gln His Ile Gln Val

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340

tgc acc ccc tgg ctg gag gcc gag gac tac ccc ctg ctt cta ggg tcg 1108

Cys Thr Pro Trp Leu Glu Ala Glu Asp Tyr Pro Leu Leu Leu Gly Ser

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350

355

gcg gac ctg ggt gtc tgt ctg cac acg tcc tcc agt ggc ctg gac ctg 1156

Ala Asp Leu Gly Val Cys Leu His Thr Ser Ser Ser Gly Leu Asp Leu

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365

370

375

ccc atg aag gtg gtg gac atg ttt ggg tgc tgt ttg cct gtg tgt gct 1204

Pro Met Lys Val Val Asp Met Phe Gly Cys Cys Leu Pro Val Cys Ala

380

385

390

gtg aac ttc aag tgt tta cat gag ctg gtg aaa cat gaa gaa aat ggc 1252

Val Asn Phe Lys Cys Leu His Glu Leu Val Lys His Glu Glu Asn Gly

395

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405

ctg gtc ttt gag gac tca gag gaa ctg gca gct cag ctg cag atg ctt 1300

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415

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ttc tca aac ttt cct gat cct gcg ggc aag cta aac cag ttc cgg aag 1348

Phe Ser Asn Phe Pro Asp Pro Ala Gly Lys Leu Asn Gln Phe Arg Lys

425

430

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aac ctg cgg gag tcg cag cag ctc cga tgg gat gag agc tgg gtg cag 1396
 Asn Leu Arg Glu Ser Gln Gln Leu Arg Trp Asp Glu Ser Trp Val Gln
 440 445 450 455

act gtg ctc cct ttg gtt atg gac aca taactcctgg gccagaggct 1443
 Thr Val Leu Pro Leu Val Met Asp Thr
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aaaagaattg gttctgtgac ccgggaagct ttggttggcc ttgatttctt ctctggaggc 1623

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accgtaagcc cagggatgtg gcagctgcag cgggcttggc tttgtgagga actgagtgtg 1863

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gtttttgg 1931

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<213> Homo sapiens

<400> 54

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Arg His Val Val Ala Val Val Leu Gly Asp Val Gly Arg Ser Pro Arg

35 40 45

Met Gln Tyr His Ala Leu Ser Leu Ala Met His Gly Phe Ser Val Thr

50 55 60

Leu Leu Gly Phe Cys Asn Ser Lys Pro His Asp Glu Leu Leu Gln Asn

65 70 75 80

~~Asn Arg Ile Gln Ile Val Gly Leu Thr Glu Leu Gln Ser Leu Ala Val~~

85 90 95

Gly Pro Arg Val Phe Gln Tyr Gly Val Lys Val Val Leu Gln Ala Met

100 105 110

Tyr Leu Leu Trp Lys Leu Met Trp Arg Glu Pro Gly Ala Tyr Ile Phe

115 120 125

Leu Gln Asn Pro Pro Gly Leu Pro Ser Ile Ala Val Cys Trp Phe Val

130

135

140

Gly Cys Leu Cys Gly Ser Lys Leu Val Ile Asp Trp His Asn Tyr Gly

145

150

155

160

Tyr Ser Ile Met Gly Leu Val His Gly Pro Asn His Pro Leu Val Leu

165

170

175

Leu Ala Lys Trp Tyr Glu Lys Phe Phe Gly Arg Leu Ser His Leu Asn

180

185

190

Leu Cys Val Thr Asn Ala Met Arg Glu Asp Leu Ala Asp Asn Trp His

195

200

205

Ile Arg Ala Val Thr Val Tyr Asp Lys Pro Ala Ser Phe Phe Lys Glu

210

215

220

Thr Pro Leu Asp Leu Gln His Arg Leu Phe Met Lys Leu Gly Ser Met

225

230

235

240

His Ser Pro Phe Arg Ala Arg Ser Glu Pro Glu Asp Pro Val Thr Glu

245

250

255

Arg Ser Ala Phe Thr Glu Arg Asp Ala Gly Ser Gly Leu Val Thr Arg

260

265

270

Leu Arg Glu Arg Pro Ala Leu Leu Val Ser Ser Thr Ser Trp Thr Glu

275

280

285

Asp Glu Asp Phe Ser Ile Leu Leu Ala Ala Leu Glu Lys Phe Glu Gln
290 295 300

Leu Thr Leu Asp Gly His Asn Leu Pro Ser Leu Val Cys Val Ile Thr
305 310 315 320

Gly Lys Gly Pro Leu Arg Glu Tyr Tyr Ser Arg Leu Ile His Gln Lys
325 330 335

His Phe Gln His Ile Gln Val Cys Thr Pro Trp Leu Glu Ala Glu Asp
340 345 350

Tyr Pro Leu Leu Leu Gly Ser Ala Asp Leu Gly Val Cys Leu His Thr
355 360 365

Ser Ser Ser Gly Leu Asp Leu Pro Met Lys Val Val Asp Met Phe Gly
370 375 380

Cys Cys Leu Pro Val Cys Ala Val Asn Phe Lys Cys Leu His Glu Leu
385 390 395 400

Val Lys His Glu Glu Asn Gly Leu Val Phe Glu Asp Ser Glu Glu Leu
405 410 415

Ala Ala Gln Leu Gln Met Leu Phe Ser Asn Phe Pro Asp Pro Ala Gly
420 425 430

Lys Leu Asn Gln Phe Arg Lys Asn Leu Arg Glu Ser Gln Gln Leu Arg

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445

Trp Asp Glu Ser Trp Val Gln Thr Val Leu Pro Leu Val Met Asp Thr

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Met Ala Ala Ala Ala Leu Pro Ala Trp Leu Ser Leu Gln

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~~tcg agg gca agg act ctg cgt gca ttc tcc act gcc gtc tac tcg gcc 98~~

Ser Arg Ala Arg Thr Leu Arg Ala Phe Ser Thr Ala Val Tyr Ser Ala

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act ccg gtc ccg aca cct agc ctg ccg gaa aga aca ccc gga aat gaa 146

Thr Pro Val Pro Thr Pro Ser Leu Pro Glu Arg Thr Pro Gly Asn Glu

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45

agg cca cca aga aga aag gca cta cct cct agg aca gag aaa atg gct 194

Arg Pro Pro Arg Arg Lys Ala Leu Pro Pro Arg Thr Glu Lys Met Ala
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gtt gac cag gac tgg cct agt gtt tac cca gtt gca gca cca ttt aaa 242
Val Asp Gln Asp Trp Pro Ser Val Tyr Pro Val Ala Ala Pro Phe Lys
65 70 75

ccc tct gca gta cct ctt cct gtt cga atg ggt tat cca gta aaa aag 290
Pro Ser Ala Val Pro Leu Pro Val Arg Met Gly Tyr Pro Val Lys Lys
80 85 90

ggc gtg ccc atg gca aag gag gga aat cta gaa ctt tta aag att ccc 338
Gly Val Pro Met Ala Lys Glu Gly Asn Leu Glu Leu Leu Lys Ile Pro
95 100 105

aat ttt ctg cat ttg act cct gta gca att aaa aag cac tgt gaa gcc 386
Asn Phe Leu His Leu Thr Pro Val Ala Ile Lys Lys His Cys Glu Ala
110 115 120 125

ctt aaa gat ttt tgc act gag tgg cca gcc gca ctg gac agt gac gag 434
~~Leu Lys Asp Phe Cys Thr Glu Trp Pro Ala Ala Leu Asp Ser Asp Glu~~

130 135 140

aaa tgt gag aag cat ttt cca att gaa att gac agc act gat tat gtt 482
Lys Cys Glu Lys His Phe Pro Ile Glu Ile Asp Ser Thr Asp Tyr Val
145 150 155

tca tca gga cca tct gtt cgg aac ccc aga gca cga gta gta gtc tta 530
Ser Ser Gly Pro Ser Val Arg Asn Pro Arg Ala Arg Val Val Val Leu

160

165

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aga gtg ccc ttt aag gag gca gaa tta cga tta tgc agt gta tct act 578

Arg Val Pro Phe Lys Glu Ala Glu Leu Arg Leu Cys Ser Val Ser Thr

175

180

185

aac agt gtt ata cca tgagtcttgg aatactgaag aatgggaaaa aagtaagact 633

Asn Ser Val Ile Pro

190

gaagcagaca tggaagagta tatatgggaa aatagctcat cagaaagaaa ttcctggaa 693

acgcttctcc agatgaaagc tgctgagaaa aatatggaaa taaataaaga agagctcctt 753

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gttt

1717

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<212> PRT

<213> Homo sapiens

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Pro Thr Pro Ser Leu Pro Glu Arg Thr Pro Gly Asn Glu Arg Pro Pro

35

40

45

Arg Arg Lys Ala Leu Pro Pro Arg Thr Glu Lys Met Ala Val Asp Gln

50

55

60

Asp Trp Pro Ser Val Tyr Pro Val Ala Ala Pro Phe Lys Pro Ser Ala

65

70

75

80

Val Pro Leu Pro Val Arg Met Gly Tyr Pro Val Lys Lys Gly Val Pro

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90

95

Met Ala Lys Glu Gly Asn Leu Glu Leu Leu Lys Ile Pro Asn Phe Leu

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His Leu Thr Pro Val Ala Ile Lys Lys His Cys Glu Ala Leu Lys Asp

115

120

125

Phe Cys Thr Glu Trp Pro Ala Ala Leu Asp Ser Asp Glu Lys Cys Glu

130

135

140

Lys His Phe Pro Ile Glu Ile Asp Ser Thr Asp Tyr Val Ser Ser Gly

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155

160

Pro Ser Val Arg Asn Pro Arg Ala Arg Val Val Val Leu Arg Val Pro

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Phe Lys Glu Ala Glu Leu Arg Leu Cys Ser Val Ser Thr Asn Ser Val

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Ile Pro

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Met Leu Met Leu Met Leu Leu

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atg atg ttt gct gtc cac tgt acc tgg gtc aca agc aat gcc tac tct 162

Met Met Phe Ala Val His Cys Thr Trp Val Thr Ser Asn Ala Tyr Ser

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agt cca agt gta gtc ctg gcc tca tac aat cat gat ggc acc agg aat 210

Ser Pro Ser Val Val Leu Ala Ser Tyr Asn His Asp Gly Thr Arg Asn

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atc tta gat gat ttt aga gaa gct tac ttt tgg cta agg caa aat aca 258

Ile Leu Asp Asp Phe Arg Glu Ala Tyr Phe Trp Leu Arg Gln Asn Thr

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gat gaa cat gca cga gta atg tct tgg tgg gat tat ggc tat cag ata 306

Asp Glu His Ala Arg Val Met Ser Trp Trp Asp Tyr Gly Tyr Gln Ile

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65

70

gct gga atg gct aat aga act acg ttg gtg gat aat aac acc tgg aat 354

Ala Gly Met Ala Asn Arg Thr Thr Leu Val Asp Asn Asn Thr Trp Asn

75

80

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aac agc cac ata gca ctg gtg gga aaa gct atg tct tct aat gaa aca 402

Asn Ser His Ile Ala Leu Val Gly Lys Ala Met Ser Ser Asn Glu Thr

90

95

100

gca gcc tat aaa atc atg agg act cta gat gta gat tat gtt ttg gtt 450

~~Ala Ala Tyr Lys Ile Met Arg Thr Leu Asp Val Asp Tyr Val Leu Val~~

105

110

115

att ttt gga ggg gtt att ggc tat tct ggt gat gat atc aac aaa ttt 498

Ile Phe Gly Gly Val Ile Gly Tyr Ser Gly Asp Asp Ile Asn Lys Phe

120

125

130

135

ctc tgg atg gtt agg ata gct gaa gga gaa cat ccc aaa gac att cgg 546

Leu Trp Met Val Arg Ile Ala Glu Gly Glu His Pro Lys Asp Ile Arg

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145

150

gaa agt gac tat ttt acc cca cag gga gaa ttc cgt gta gac aaa gca 594

Glu Ser Asp Tyr Phe Thr Pro Gln Gly Glu Phe Arg Val Asp Lys Ala

155

160

165

gga tcc cct act ttg ttg aat tgc ctt atg tat aaa atg tca tac tac 642

Gly Ser Pro Thr Leu Leu Asn Cys Leu Met Tyr Lys Met Ser Tyr Tyr

170

175

180

aga ttt gga gaa atg cag ctg gat ttt cgt aca ccc cca ggt ttt gac 690

Arg Phe Gly Glu Met Gln Leu Asp Phe Arg Thr Pro Pro Gly Phe Asp

185

190

195

cga aca cgt aat gct gag att gga aat aag gac att aaa ttc aaa cat 738

Arg Thr Arg Asn Ala Glu Ile Gly Asn Lys Asp Ile Lys Phe Lys His

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Leu Glu Glu Ala Phe Thr Ser Glu His Trp Leu Val Arg Ile Tyr Lys

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gta aaa gca cct gat aac agg gag aca tta gat cac aaa cct cga gtc 834

Val Lys Ala Pro Asp Asn Arg Glu Thr Leu Asp His Lys Pro Arg Val

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240

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acc aac att ttc cca aaa cag aag tat ttg tca aag aag act acc aaa 882

Thr Asn Ile Phe Pro Lys Gln Lys Tyr Leu Ser Lys Lys Thr Thr Lys

250

255

260

agg aag cgt ggc tac att aaa aat aag ctg gtt ttt aag aaa ggc aag 930

Arg Lys Arg Gly Tyr Ile Lys Asn Lys Leu Val Phe Lys Lys Gly Lys

265

270

275

aaa ata tct aag aag act gtt taaatgcact gttctgggtc ctaacttgaa 981

Lys Ile Ser Lys Lys Thr Val

280

285

gcagttgtcc ttgtgagaac cggctctttgc ctttagctca tgctgtgttt cacagcaaag 1041

agggtacaga accatcactg gtccagggtta atgtacaaaa ttttctggca atgcctgatt 1101

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cccttaagca tttgatgaaa cactcttttag tgctatatgc attttcttac tttgttaaa 2001

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atttacaata ttcagtgaga atgttactgc tgattttctt ttccaagggtg tagaatattc 2301

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gctgaacatt ttcacaaata gagtgaacg aagtctggat ttctgatacc ttgtcatttg 2421

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2510

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<211> 286

<212> PRT

<213> Homo sapiens

<400> 58

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10

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Val Thr Ser Asn Ala Tyr Ser Ser Pro Ser Val Val Leu Ala Ser Tyr

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25

30

Asn His Asp Gly Thr Arg Asn Ile Leu Asp Asp Phe Arg Glu Ala Tyr

35

40

45

Phe Trp Leu Arg Gln Asn Thr Asp Glu His Ala Arg Val Met Ser Trp

50

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Trp Asp Tyr Gly Tyr Gln Ile Ala Gly Met Ala Asn Arg Thr Thr Leu

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Val Asp Asn Asn Thr Trp Asn Asn Ser His Ile Ala Leu Val Gly Lys

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95

Ala Met Ser Ser Asn Glu Thr Ala Ala Tyr Lys Ile Met Arg Thr Leu

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105

110

Asp Val Asp Tyr Val Leu Val Ile Phe Gly Gly Val Ile Gly Tyr Ser

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Gly Asp Asp Ile Asn Lys Phe Leu Trp Met Val Arg Ile Ala Glu Gly

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Glu His Pro Lys Asp Ile Arg Glu Ser Asp Tyr Phe Thr Pro Gln Gly

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Glu Phe Arg Val Asp Lys Ala Gly Ser Pro Thr Leu Leu Asn Cys Leu

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Met Tyr Lys Met Ser Tyr Tyr Arg Phe Gly Glu Met Gln Leu Asp Phe

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Arg Thr Pro Pro Gly Phe Asp Arg Thr Arg Asn Ala Glu Ile Gly Asn

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Lys Asp Ile Lys Phe Lys His Leu Glu Glu Ala Phe Thr Ser Glu His

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Trp Leu Val Arg Ile Tyr Lys Val Lys Ala Pro Asp Asn Arg Glu Thr

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Leu Asp His Lys Pro Arg Val Thr Asn Ile Phe Pro Lys Gln Lys Tyr

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~~Met-Leu-Leu-Leu-Leu-Gly-Leu-Cys-Leu-Gly-Leu~~

1

5

10

tcc ctg tgt gtg ggg tcg cag gaa gag gcg cag agc tgg ggc cac tct 160

Ser Leu Cys Val Gly Ser Gln Glu Glu Ala Gln Ser Trp Gly His Ser

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Ser Glu Gln Asp Gly Leu Arg Val Pro Arg Gln Val Arg Leu Leu Gln

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Arg Leu Lys Thr Lys Pro Leu Met Thr Glu Phe Ser Val Lys Ser Thr

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Ile Ile Ser Arg Tyr Ala Phe Thr Thr Val Pro Cys Arg Met Leu Asn

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aga gct tct gaa gac cag gac att gag ttc cag atg cag att cca gct 352

Arg Ala Ser Glu Asp Gln Asp Ile Glu Phe Gln Met Gln Ile Pro Ala

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Ala Ala Phe Ile Thr Asn Phe Thr Met Leu Ile Gly Asp Lys Val Tyr

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Gln Gly Glu Ile Thr Glu Arg Glu Lys Lys Ser Gly Asp Arg Val Lys

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Glu Lys Arg Asn Lys Thr Thr Glu Glu Asn Gly Glu Lys Gly Thr Glu

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Ile Phe Arg Ala Ser Ala Val Ile Pro Ser Lys Asp Lys Ala Ala Phe

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ttc ctg agt tat gag gag ctt ctg cag agg cgc ctg ggc aag tac gag 592

Phe Leu Ser Tyr Glu Glu Leu Leu Gln Arg Arg Leu Gly Lys Tyr Glu

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His Ser Ile Ser Val Arg Pro Gln Gln Leu Ser Gly Arg Leu Ser Val

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gac gtg aat atc ctg gag agc gcg ggc atc gca tcc ctg gag gtg ctg 688

Asp Val Asn Ile Leu Glu Ser Ala Gly Ile Ala Ser Leu Glu Val Leu

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ccg ctt cac aac agc agg cag agg ggc agt ggg cgc ggg gaa gat gat 736

Pro Leu His Asn Ser Arg Gln Arg Gly Ser Gly Arg Gly Glu Asp Asp

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Ser Gly Pro Pro Pro Ser Thr Val Ile Asn Gln Asn Glu Thr Phe Ala

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aac ata att ttt aaa cct act gta gta caa caa gcc agg att gcc cag 832

Asn Ile Ile Phe Lys Pro Thr Val Val Gln Gln Ala Arg Ile Ala Gln

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aat gga ttt ttg gga gac ttt atc att aga tat gac gtc aat aga gaa 880

Asn Gly Phe Leu Gly Asp Phe Ile Ile Arg Tyr Asp Val Asn Arg Glu

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cag agc att ggg gac atc cag gtt cta aat ggc tat ttt gtg cac tac 928
Gln Ser Ile Gly Asp Ile Gln Val Leu Asn Gly Tyr Phe Val His Tyr

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ttt gct cct aaa gac ctt cct cct tta ccc aag aat gtg gta ttc gtg 976
Phe Ala Pro Lys Asp Leu Pro Pro Leu Pro Lys Asn Val Val Phe Val

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gat gcc ctc ttc aca att ctc cat gac ctc cga ccc cag gac cgt ttc 1072
Asp Ala Leu Phe Thr Ile Leu His Asp Leu Arg Pro Gln Asp Arg Phe

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Ile Ser Val Thr Pro Asp Ser Ile Arg Asp Gly Asn Val Tyr Ile His

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His Met Ser Pro Thr Gly Gly Thr Asp Ile Asn Gly Ala Leu Gln Arg

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Ala Ile Arg Leu Leu Asn Lys Tyr Val Ala His Ser Gly Ile Gly Asp
380 385 390 395

cgg agc gtg tcc ctc atc gtc ttc ctg acg gat ggg aag ccc acg gtc 1312
Arg Ser Val Ser Leu Ile Val Phe Leu Thr Asp Gly Lys Pro Thr Val
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ggg gag acg cac acc ctc aag atc ctc aac aac acc cga gag gcc gcc 1360
Gly Glu Thr His Thr Leu Lys Ile Leu Asn Asn Thr Arg Glu Ala Ala
415 420 425

cga ggc caa gtc tgc atc ttc acc att ggc atc ggc aac gac gtg gac 1408
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Arg Val His Glu Glu Glu Asp Ala Gly Ser Gln Leu Ile Gly Phe Tyr
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gat gaa atc agg acc ccg ctc ctc tct gac atc cgc atc gat tat ccc 1552
Asp Glu Ile Arg Thr Pro Leu Leu Ser Asp Ile Arg Ile Asp Tyr Pro
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Pro Ser Ser Val Val Gln Ala Thr Lys Thr Leu Phe Pro Asn Tyr Phe

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aac ggc tcg gag atc atc att gcg ggg aag ctg gtg gac agg aag ctg 1648

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Asp His Leu His Val Glu Val Thr Ala Ser Asn Ser Lys Lys Phe Ile

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atc ctg aag aca gat gtg cct gtg cgg cct cag aag gca ggg aaa gat 1744

Ile Leu Lys Thr Asp Val Pro Val Arg Pro Gln Lys Ala Gly Lys Asp

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Val Thr Gly Ser Pro Arg Pro Gly Gly Asp Gly Glu Gly Asp Pro Asn

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His Ile Glu Arg Leu Trp Ser Tyr Leu Thr Thr Lys Glu Leu Leu Ser

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tcc tgg ctg caa agt gac gat gaa ccg gag aag gag cgg ctg cgg cag 1888

Ser Trp Leu Gln Ser Asp Asp Glu Pro Glu Lys Glu Arg Leu Arg Gln

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cgg gcc cag gcc ctg gct gtg agc tac cgc ttc ctc act ccc ttc acc 1936

Arg Ala Gln Ala Leu Ala Val Ser Tyr Arg Phe Leu Thr Pro Phe Thr

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 Ser Met Lys Leu Arg Gly Pro Val Pro Arg Met Asp Gly Leu Glu Glu
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gcc cac ggc atg tcg gct gcc atg gga ccc gaa ccg gtg gtg cag agc 2032
 Ala His Gly Met Ser Ala Ala Met Gly Pro Glu Pro Val Val Gln Ser
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gtg cga gga gct ggc acg cag cca gga cct ttg ctc aag aag cca tac 2080
 Val Arg Gly Ala Gly Thr Gln Pro Gly Pro Leu Leu Lys Lys Pro Tyr
 655 660 665

cag cca aga att aaa atc tct aaa aca tca gtg gat ggt gat ccc cac 2128
 Gln Pro Arg Ile Lys Ile Ser Lys Thr Ser Val Asp Gly Asp Pro His
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ttt gtt gtg gat ttc ccc ctg agc aga ctc acc gtg tgc ttc aac att 2176
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 685 690 695

gat ggg cag ccc ggg gac atc ctc agg ctg gtc tct gat cac agg gac 2224
 Asp Gly Gln Pro Gly Asp Ile Leu Arg Leu Val Ser Asp His Arg Asp
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tct ggt gtc aca gtg aac gga gag tta att ggg gca ccc gcc cct cca 2272
 Ser Gly Val Thr Val Asn Gly Glu Leu Ile Gly Ala Pro Ala Pro Pro
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aat ggc cac aag aaa cag cgc act tac ttg cgc act atc acc atc ctc 2320

Asn Gly His Lys Lys Gln Arg Thr Tyr Leu Arg Thr Ile Thr Ile Leu

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atc aac aag cca gag aga tct tat ctc gag atc aca ccg agc aga gtc 2368

Ile Asn Lys Pro Glu Arg Ser Tyr Leu Glu Ile Thr Pro Ser Arg Val

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Ile Leu Asp Gly Gly Asp Arg Leu Val Leu Pro Cys Asn Gln Ser Val

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Val Val Gly Ser Trp Gly Leu Glu Val Ser Val Ser Ala Asn Ala Asn

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gtc acc gtc acc atc cag ggc tcc ata gcc ttt gtc atc ctc atc cac 2512

Val Thr Val Thr Ile Gln Gly Ser Ile Ala Phe Val Ile Leu Ile His

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ctc tac aaa aag ccg ggc gcc ctt cca gcg aca cca cct ggg ttt cta 2560

Leu Tyr Lys Lys Pro Gly Ala Leu Pro Ala Thr Pro Pro Gly Phe Leu

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cat tgc caa cag cga ggg cct ttc cag caa ctg cca cgg act gct ggg 2608

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835

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Ser Val Pro Glu Ser Gly Cys Gln Thr His Arg Arg Pro Cys Arg Ala

845

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cag cca gaa cct cac tca ccc tct gct cct tca ggt ggg aga ggg gcc 2704

Gln Pro Glu Pro His Ser Pro Ser Ala Pro Ser Gly Gly Arg Gly Ala

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865

870

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35 40 45

Pro Leu Met Thr Glu Phe Ser Val Lys Ser Thr Ile Ile Ser Arg Tyr

50 55 60

Ala Phe Thr Thr Val Pro Cys Arg Met Leu Asn Arg Ala Ser Glu Asp

65 70 75 80

Gln Asp Ile Glu Phe Gln Met Gln Ile Pro Ala Ala Ala Phe Ile Thr

85

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Asn Phe Thr Met Leu Ile Gly Asp Lys Val Tyr Gln Gly Glu Ile Thr

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Glu Arg Glu Lys Lys Ser Gly Asp Arg Val Lys Glu Lys Arg Asn Lys

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Thr Thr Glu Glu Asn Gly Glu Lys Gly Thr Glu Ile Phe Arg Ala Ser

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Ala Val Ile Pro Ser Lys Asp Lys Ala Ala Phe Phe Leu Ser Tyr Glu

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Glu Leu Leu Gln Arg Arg Leu Gly Lys Tyr Glu His Ser Ile Ser Val

165

170

175

Arg Pro Gln Gln Leu Ser Gly Arg Leu Ser Val Asp Val Asn Ile Leu

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185

190

Glu Ser Ala Gly Ile Ala Ser Leu Glu Val Leu Pro Leu His Asn Ser

195

200

205

Arg Gln Arg Gly Ser Gly Arg Gly Glu Asp Asp Ser Gly Pro Pro Pro

210

215

220

Ser Thr Val Ile Asn Gln Asn Glu Thr Phe Ala Asn Ile Ile Phe Lys



225 230 235 240

Pro Thr Val Val Gln Gln Ala Arg Ile Ala Gln Asn Gly Phe Leu Gly

245 250 255

Asp Phe Ile Ile Arg Tyr Asp Val Asn Arg Glu Gln Ser Ile Gly Asp

260 265 270

Ile Gln Val Leu Asn Gly Tyr Phe Val His Tyr Phe Ala Pro Lys Asp

275 280 285

Leu Pro Pro Leu Pro Lys Asn Val Val Phe Val Leu Asp Ser Ser Ala

290 295 300

Pro Met Val Gly Thr Lys Leu Arg Gln Thr Lys Asp Ala Leu Phe Thr

305 310 315 320

Ile Leu His Asp Leu Arg Pro Gln Asp Arg Phe Ser Ile Ile Gly Phe

325 330 335

Ser Asn Arg Ile Lys Val Trp Lys Asp His Leu Ile Ser Val Thr Pro

340 345 350

Asp Ser Ile Arg Asp Gly Asn Val Tyr Ile His His Met Ser Pro Thr

355 360 365

Gly Gly Thr Asp Ile Asn Gly Ala Leu Gln Arg Ala Ile Arg Leu Leu

370 375 380

Asn Lys Tyr Val Ala His Ser Gly Ile Gly Asp Arg Ser Val Ser Leu
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Ile Val Phe Leu Thr Asp Gly Lys Pro Thr Val Gly Glu Thr His Thr
405 410 415

Leu Lys Ile Leu Asn Asn Thr Arg Glu Ala Ala Arg Gly Gln Val Cys
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Ile Phe Thr Ile Gly Ile Gly Asn Asp Val Asp Phe Arg Leu Leu Glu
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Lys Leu Ser Leu Glu Asn Cys Gly Leu Thr Arg Arg Val His Glu Glu
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Glu Asp Ala Gly Ser Gln Leu Ile Gly Phe Tyr Asp Glu Ile Arg Thr
465 470 475 480

Pro Leu Leu Ser Asp Ile Arg Ile Asp Tyr Pro Pro Ser Ser Val Val
485 490 495

Gln Ala Thr Lys Thr Leu Phe Pro Asn Tyr Phe Asn Gly Ser Glu Ile
500 505 510

Ile Ile Ala Gly Lys Leu Val Asp Arg Lys Leu Asp His Leu His Val
515 520 525

Glu Val Thr Ala Ser Asn Ser Lys Lys Phe Ile Ile Leu Lys Thr Asp
530 535 540

Val Pro Val Arg Pro Gln Lys Ala Gly Lys Asp Val Thr Gly Ser Pro
545 550 555 560

Arg Pro Gly Gly Asp Gly Glu Gly Asp Pro Asn His Ile Glu Arg Leu
565 570 575

Trp Ser Tyr Leu Thr Thr Lys Glu Leu Leu Ser Ser Trp Leu Gln Ser
580 585 590

Asp Asp Glu Pro Glu Lys Glu Arg Leu Arg Gln Arg Ala Gln Ala Leu
595 600 605

Ala Val Ser Tyr Arg Phe Leu Thr Pro Phe Thr Ser Met Lys Leu Arg
610 615 620

Gly Pro Val Pro Arg Met Asp Gly Leu Glu Glu Ala His Gly Met Ser
625 630 635 640

Ala Ala Met Gly Pro Glu Pro Val Val Gln Ser Val Arg Gly Ala Gly
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Thr Gln Pro Gly Pro Leu Leu Lys Lys Pro Tyr Gln Pro Arg Ile Lys
660 665 670

Ile Ser Lys Thr Ser Val Asp Gly Asp Pro His Phe Val Val Asp Phe
675 680 685

Pro Leu Ser Arg Leu Thr Val Cys Phe Asn Ile Asp Gly Gln Pro Gly

690

695

700

Asp Ile Leu Arg Leu Val Ser Asp His Arg Asp Ser Gly Val Thr Val

705

710

715

720

Asn Gly Glu Leu Ile Gly Ala Pro Ala Pro Pro Asn Gly His Lys Lys

725

730

735

Gln Arg Thr Tyr Leu Arg Thr Ile Thr Ile Leu Ile Asn Lys Pro Glu

740

745

750

Arg Ser Tyr Leu Glu Ile Thr Pro Ser Arg Val Ile Leu Asp Gly Gly

755

760

765

Asp Arg Leu Val Leu Pro Cys Asn Gln Ser Val Val Val Gly Ser Trp

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775

780

Gly Leu Glu Val Ser Val Ser Ala Asn Ala Asn Val Thr Val Thr Ile

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790

795

800

Gln Gly Ser Ile Ala Phe Val Ile Leu Ile His Leu Tyr Lys Lys Pro

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825

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Gly Pro Phe Gln Gln Leu Pro Arg Thr Ala Gly Ser Val Pro Glu Ser

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 Met Ala Val Phe Val
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 Val Leu Leu Ala Leu Val Ala Gly Val Leu Gly Asn Glu Phe Ser Ile
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Leu Lys Ser Pro Gly Ser Val Val Phe Arg Asn Gly Asn Trp Pro Ile

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cca gga gag cgg atc cca gac gtg gct gca ttg tcc atg ggc ttc tct 319

Pro Gly Glu Arg Ile Pro Asp Val Ala Ala Leu Ser Met Gly Phe Ser

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Val Lys Glu Asp Leu Ser Trp Pro Gly Leu Ala Val Gly Asn Leu Phe

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His Arg Pro Arg Ala Thr Val Met Val Met Val Lys Gly Val Asn Lys

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Leu Ala Leu Pro Pro Gly Ser Val Ile Ser Tyr Pro Leu Glu Asn Ala

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95

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gtt cct ttt agt ctt gac agt gtt gca aat tcc att cac tcc tta ttt 511

Val Pro Phe Ser Leu Asp Ser Val Ala Asn Ser Ile His Ser Leu Phe

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Ser Glu Glu Thr Pro Val Val Leu Gln Leu Ala Pro Ser Glu Glu Arg

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Val Tyr Met Val Gly Lys Ala Asn Ser Val Phe Glu Asp Leu Ser Val
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acc ttg cgc cag ctc cgt aat cgc ctg ttt caa gaa aac tct gtt ctc 655
Thr Leu Arg Gln Leu Arg Asn Arg Leu Phe Gln Glu Asn Ser Val Leu
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Ser Ser Leu Pro Leu Asn Ser Leu Ser Arg Asn Asn Glu Val Asp Leu
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ctc ttt ctt tct gaa ctg caa gtg cta cat gat att tca agc ttg ctg 751
Leu Phe Leu Ser Glu Leu Gln Val Leu His Asp Ile Ser Ser Leu Leu
185 190 195

tct cgt cat aag cat cta gcc aag gat cat tct cct gat tta tat tca 799
Ser Arg His Lys His Leu Ala Lys Asp His Ser Pro Asp Leu Tyr Ser
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Leu Glu Leu Ala Gly Leu Asp Glu Ile Gly Lys Arg Tyr Gly Glu Asp

215 220 225

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Asn Leu Ala Tyr Lys Tyr Asn Phe Glu Tyr Ser Val Val Phe Asn Met

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Val Leu Trp Ile Met Ile Ala Leu Ala Leu Ala Val Ile Ile Thr Ser

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325

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Met Thr Asn Gln Lys Ile Arg Met Asp

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gttttttaac cctcttctgc aagtttggtg acctacatgg gctaatatgg atactaaaaa 1830

tactacattg atctaagaag aaactagcct tgtggagtat atagatgctt ttcattatac 1890

acacaaaaat cctgagggga cttttgagg catgaatata aaacattttt atttcagtaa 1950

ctttccccc tgtgtaagtt actatggttt gtggtacaac ttcattctat agaataattaa 2010

gtggaagtgg gtgaattcta ctttttatgt tggagtggac caatgtctat caagagtgc 2070

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<211> 350

<212> PRT

<213> Homo sapiens

<400> 62

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Asn Glu Phe Ser Ile Leu Lys Ser Pro Gly Ser Val Val Phe Arg Asn

20 25 30

Gly Asn Trp Pro Ile Pro Gly Glu Arg Ile Pro Asp Val Ala Ala Leu

35 40 45

Ser Met Gly Phe Ser Val Lys Glu Asp Leu Ser Trp Pro Gly Leu Ala

50 55 60

Val Gly Asn Leu Phe His Arg Pro Arg Ala Thr Val Met Val Met Val

65 70 75 80

~~Lys Gly Val Asn Lys Leu Ala Leu Pro Pro Gly Ser Val Ile Ser Tyr~~

85 90 95

Pro Leu Glu Asn Ala Val Pro Phe Ser Leu Asp Ser Val Ala Asn Ser

100 105 110

Ile His Ser Leu Phe Ser Glu Glu Thr Pro Val Val Leu Gln Leu Ala

115 120 125

Pro Ser Glu Glu Arg Val Tyr Met Val Gly Lys Ala Asn Ser Val Phe
130 135 140

Glu Asp Leu Ser Val Thr Leu Arg Gln Leu Arg Asn Arg Leu Phe Gln
145 150 155 160

Glu Asn Ser Val Leu Ser Ser Leu Pro Leu Asn Ser Leu Ser Arg Asn
165 170 175

Asn Glu Val Asp Leu Leu Phe Leu Ser Glu Leu Gln Val Leu His Asp
180 185 190

Ile Ser Ser Leu Leu Ser Arg His Lys His Leu Ala Lys Asp His Ser
195 200 205

Pro Asp Leu Tyr Ser Leu Glu Leu Ala Gly Leu Asp Glu Ile Gly Lys
210 215 220

Arg Tyr Gly Glu Asp Ser Glu Gln Phe Arg Asp Ala Ser Lys Ile Leu
225 230 235 240

Val Asp Ala Leu Gln Lys Phe Ala Asp Asp Met Tyr Ser Leu Tyr Gly
245 250 255

Gly Lys Ala Val Val Glu Leu Val Thr Val Lys Ser Phe Asp Thr Ser
260 265 270

Leu Ile Arg Lys Thr Arg Thr Ile Leu Glu Ala Lys Gln Ala Lys Asn
275 280 285

Pro Ala Ser Pro Tyr Asn Leu Ala Tyr Lys Tyr Asn Phe Glu Tyr Ser
290 295 300

Val Val Phe Asn Met Val Leu Trp Ile Met Ile Ala Leu Ala Leu Ala
305 310 315 320

Val Ile Ile Thr Ser Tyr Asn Ile Trp Asn Met Asp Pro Gly Tyr Asp
325 330 335

Ser Ile Ile Tyr Arg Met Thr Asn Gln Lys Ile Arg Met Asp
340 345 350

<210> 63

<211> 2341

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<222> (94)..(1662)

<400> 63

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Met Ala Gly Gln Arg Val Leu

1

5

ctt cta gtg ggc ttc ctt ctc cct ggg gtc ctg ctc tca gag gct gcc 162

Leu Leu Val Gly Phe Leu Leu Pro Gly Val Leu Leu Ser Glu Ala Ala

10

15

20

aaa atc ctg aca ata tct aca gta ggt gga agc cat tat cta ctg atg 210

Lys Ile Leu Thr Ile Ser Thr Val Gly Gly Ser His Tyr Leu Leu Met

25

30

35

gac cgg gtt tct cag att ctt caa gat cac ggt cat aat gtc acc atg 258

Asp Arg Val Ser Gln Ile Leu Gln Asp His Gly His Asn Val Thr Met

40

45

50

55

ctt aac cac aaa aga ggt cct ttt atg cca gat ttt aaa aag gaa gaa 306

Leu Asn His Lys Arg Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu

60

65

70

aaa tca tat caa gtt atc agt tgg ctt gca cct gaa gat cat caa aga 354

Lys Ser Tyr Gln Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg

75

80

85

gaa ttt aaa aag agt ttt gat ttc ttt ctg gaa gaa act tta ggt ggc 402

Glu Phe Lys Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly

90

95

100

aga gga aaa ttt gaa aac tta tta aat gtt cta gaa tac ttg gcg ttg 450

Arg Gly Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu

105

110

115

cag tgc agt cat ttt tta aat aga aag gat atc atg gat tcc tta aag 498

Gln Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys

120 125 130 135

aat gag aac ttc gac atg gtg ata gtt gaa act ttt gac tac tgt cct 546

Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys Pro

140 145 150

ttc ctg att gct gag aag ctt ggg aag cca ttt gtg gcc att ctt tcc 594

Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile Leu Ser

155 160 165

act tca ttc ggc tct ttg gaa ttt ggg cta cca atc ccc ttg tct tat 642

Thr Ser Phe Gly Ser Leu Glu Phe Gly Leu Pro Ile Pro Leu Ser Tyr

170 175 180

gtt cca gta ttc cgt tcc ttg ctg act gat cac atg gac ttc tgg ggc 690

Val Pro Val Phe Arg Ser Leu Leu Thr Asp His Met Asp Phe Trp Gly

185 190 195

~~cga gtg aag aat ttt ctg atg ttc ttt agt ttc tgc agg agg caa cag 738~~

Arg Val Lys Asn Phe Leu Met Phe Phe Ser Phe Cys Arg Arg Gln Gln

200 205 210 215

cac atg cag tct aca ttt gac aac acc atc aag gaa cat ttc aca gaa 786

His Met Gln Ser Thr Phe Asp Asn Thr Ile Lys Glu His Phe Thr Glu

220 225 230

ggc tct agg cca gtt ttg tct cat ctt cta ctg aaa gca gag ttg tgg 834

Gly Ser Arg Pro Val Leu Ser His Leu Leu Leu Lys Ala Glu Leu Trp

235

240

245

ttc att aac tct gac ttt gcc ttt gat ttt gct cga cct ctg ctt ccc 882

Phe Ile Asn Ser Asp Phe Ala Phe Asp Phe Ala Arg Pro Leu Leu Pro

250

255

260

aac act gtt tat gtt gga ggc ttg atg gaa aaa cct att aaa cca gta 930

Asn Thr Val Tyr Val Gly Gly Leu Met Glu Lys Pro Ile Lys Pro Val

265

270

275

cca caa gac ttg gag aac ttc att gcc aag ttt gag gac tct ggt ttt 978

Pro Gln Asp Leu Glu Asn Phe Ile Ala Lys Phe Glu Asp Ser Gly Phe

280

285

290

295

gtc ctt gtg acc ttg ggc tcc atg gtg aac acc tgt cag aat ccg gaa 1026

Val Leu Val Thr Leu Gly Ser Met Val Asn Thr Cys Gln Asn Pro Glu

300

305

310

atc ttc aag gag atg aac aat gcc ttt gct cac cta ccc caa ggg gtg 1074

Ile Phe Lys Glu Met Asn Asn Ala Phe Ala His Leu Pro Gln Gly Val

315

320

325

ata tgg aag tgt cag tgt tct cat tgg ccc aaa gat gtc cac ctg gct 1122

Ile Trp Lys Cys Gln Cys Ser His Trp Pro Lys Asp Val His Leu Ala

330

335

340

gca aat gtg aaa att gtg gac tgg ctt cct cag agt gac ctc ctg gct 1170

Ala Asn Val Lys Ile Val Asp Trp Leu Pro Gln Ser Asp Leu Leu Ala

345

350

355

cac cca agc atc cgt ctg ttt gtc acc cac ggc ggg cag aat agc ata 1218
His Pro Ser Ile Arg Leu Phe Val Thr His Gly Gly Gln Asn Ser Ile
360 365 370 375

atg gag gcc atc cag cat ggt gtg ccc atg gtg ggg atc cct ctc ttt 1266
Met Glu Ala Ile Gln His Gly Val Pro Met Val Gly Ile Pro Leu Phe
380 385 390

gga gac cag cct gaa aac atg gtc cga gta gaa gcc aaa aag ttt ggt 1314
Gly Asp Gln Pro Glu Asn Met Val Arg Val Glu Ala Lys Lys Phe Gly
395 400 405

gtt tct att cag tta aag aag ctc aag gca gag aca ttg gct ctt aag 1362
Val Ser Ile Gln Leu Lys Lys Leu Lys Ala Glu Thr Leu Ala Leu Lys
410 415 420

atg aaa caa atc atg gaa gac aag aga tac aag tcc gcg gca gtg gct 1410
Met Lys Gln Ile Met Glu Asp Lys Arg Tyr Lys Ser Ala Ala Val Ala
425 430 435

gcc agt gtc atc ctg cgc tcc cac ccg ctc agc ccc aca cag cgg ctg 1458
Ala Ser Val Ile Leu Arg Ser His Pro Leu Ser Pro Thr Gln Arg Leu
440 445 450 455

gtg ggc tgg att gac cac gtc ctc cag aca ggg ggc gcg acg cac ctc 1506
Val Gly Trp Ile Asp His Val Leu Gln Thr Gly Gly Ala Thr His Leu
460 465 470

aag ccc tat gtc ttt cag cag ccc tgg cat gag cag tac ctg ctc gac 1554

Lys Pro Tyr Val Phe Gln Gln Pro Trp His Glu Gln Tyr Leu Leu Asp

475

480

485

gtt ttt gtg ttt ctg ctg ggg ctc act ctg ggg act cta tgg ctt tgt 1602

Val Phe Val Phe Leu Leu Gly Leu Thr Leu Gly Thr Leu Trp Leu Cys

490

495

500

ggg aag ctg ctg ggc atg gct gtc tgg tgg ctg cgt ggg gcc aga aag 1650

Gly Lys Leu Leu Gly Met Ala Val Trp Trp Leu Arg Gly Ala Arg Lys

505

510

515

gtg aag gag aca taaggccagg tgcagccttg gcggggtctg tttggtgggc 1702

Val Lys Glu Thr

520

gatgtcacca tttctaggga gcttcccact agttctggca gcccattct ctagtccttc 1762

tagttatctc ctgttttctt gaagaacagg aaaaatggcc aaaaatcatc ctttccactt 1822

gctaattttg ctacaaattc atccttacta gctcctgcct gctagcagaa ttctttccag 1882

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gacttggacc actgaccctc agatttccag ccttaaaatc caccttcctt ctcatgcgcc 2002

tctccgaatc acaccctgac tcttccagcc tccatgtcca gacctagtca gcctctctca 2062

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cagtttctgt ttgtttctcc cacatattct cttcaatgct caggaagcct gccctgtgct 2182

tgagagtcca gggccggaca caggctcaca ggtctccaca ttgggtccct gtctctggtg 2242

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<211> 523

<212> PRT

<213> Homo sapiens

<400> 64

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Val Leu Leu Ser Glu Ala Ala Lys Ile Leu Thr Ile Ser Thr Val Gly

20 25 30

Gly Ser His Tyr Leu Leu Met Asp Arg Val Ser Gln Ile Leu Gln Asp

35 40 45

His Gly His Asn Val Thr Met Leu Asn His Lys Arg Gly Pro Phe Met

50 55 60



Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln Val Ile Ser Trp Leu
65 70 75 80

Ala Pro Glu Asp His Gln Arg Glu Phe Lys Lys Ser Phe Asp Phe Phe
85 90 95

Leu Glu Glu Thr Leu Gly Gly Arg Gly Lys Phe Glu Asn Leu Leu Asn
100 105 110

Val Leu Glu Tyr Leu Ala Leu Gln Cys Ser His Phe Leu Asn Arg Lys
115 120 125

Asp Ile Met Asp Ser Leu Lys Asn Glu Asn Phe Asp Met Val Ile Val
130 135 140

Glu Thr Phe Asp Tyr Cys Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys
145 150 155 160

Pro Phe Val Ala Ile Leu Ser Thr Ser Phe Gly Ser Leu Glu Phe Gly
165 170 175

Leu Pro Ile Pro Leu Ser Tyr Val Pro Val Phe Arg Ser Leu Leu Thr
180 185 190

Asp His Met Asp Phe Trp Gly Arg Val Lys Asn Phe Leu Met Phe Phe
195 200 205

Ser Phe Cys Arg Arg Gln Gln His Met Gln Ser Thr Phe Asp Asn Thr
210 215 220

Ile Lys Glu His Phe Thr Glu Gly Ser Arg Pro Val Leu Ser His Leu
225 230 235 240

Leu Leu Lys Ala Glu Leu Trp Phe Ile Asn Ser Asp Phe Ala Phe Asp
245 250 255

Phe Ala Arg Pro Leu Leu Pro Asn Thr Val Tyr Val Gly Gly Leu Met
260 265 270

Glu Lys Pro Ile Lys Pro Val Pro Gln Asp Leu Glu Asn Phe Ile Ala
275 280 285

Lys Phe Glu Asp Ser Gly Phe Val Leu Val Thr Leu Gly Ser Met Val
290 295 300

Asn Thr Cys Gln Asn Pro Glu Ile Phe Lys Glu Met Asn Asn Ala Phe
305 310 315 320

Ala His Leu Pro Gln Gly Val Ile Trp Lys Cys Gln Cys Ser His Trp
325 330 335

Pro Lys Asp Val His Leu Ala Ala Asn Val Lys Ile Val Asp Trp Leu
340 345 350

Pro Gln Ser Asp Leu Leu Ala His Pro Ser Ile Arg Leu Phe Val Thr
355 360 365

His Gly Gly Gln Asn Ser Ile Met Glu Ala Ile Gln His Gly Val Pro

370	375	380	
Met Val Gly Ile Pro Leu Phe Gly Asp Gln Pro Glu Asn Met Val Arg			
385	390	395	400
Val Glu Ala Lys Lys Phe Gly Val Ser Ile Gln Leu Lys Lys Leu Lys			
405	410	415	
Ala Glu Thr Leu Ala Leu Lys Met Lys Gln Ile Met Glu Asp Lys Arg			
420	425	430	
Tyr Lys Ser Ala Ala Val Ala Ala Ser Val Ile Leu Arg Ser His Pro			
435	440	445	
Leu Ser Pro Thr Gln Arg Leu Val Gly Trp Ile Asp His Val Leu Gln			
450	455	460	
Thr Gly Gly Ala Thr His Leu Lys Pro Tyr Val Phe Gln Gln Pro Trp			
465	470	475	480
<hr/>			
His Glu Gln Tyr Leu Leu Asp Val Phe Val Phe Leu Leu Gly Leu Thr			
485	490	495	
Leu Gly Thr Leu Trp Leu Cys Gly Lys Leu Leu Gly Met Ala Val Trp			
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Trp Leu Arg Gly Ala Arg Lys Val Lys Glu Thr			
515	520		

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<211> 2971

<212> DNA

<213> Homo sapiens

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<222> (103)..(2412)

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Met Pro Ala Ser

1

gct gcg cgg ccc cgc ccg ggt ccc ggg cag cct aca gcc tcg ccc ttc 162

Ala Ala Arg Pro Arg Pro Gly Pro Gly Gln Pro Thr Ala Ser Pro Phe

5

10

15

20

ccg cta ctg ctg ctg gcg gtg ctg agc ggc ccg gta tcc ggc cgc gtc 210

Pro Leu Leu Leu Leu Ala Val Leu Ser Gly Pro Val Ser Gly Arg Val

25

30

35

ccc cgc tcg gtg ccc aga acc tcg ctt cca atc tct gag gct gac tcc 258

Pro Arg Ser Val Pro Arg Thr Ser Leu Pro Ile Ser Glu Ala Asp Ser

40

45

50

tgt ctc acc cgg ttc gca gtc cct cac aca tac aat tac tct gtt ctc 306

Cys Leu Thr Arg Phe Ala Val Pro His Thr Tyr Asn Tyr Ser Val Leu

55

60

65

ctt gtg gat cct gcc tcc cac aca ctt tat gtt ggc gcc cgg gac acc 354

Leu Val Asp Pro Ala Ser His Thr Leu Tyr Val Gly Ala Arg Asp Thr

70

75

80

atc ttc gct tta tcc ctg ccc ttc tca ggg gag aga ccc cgc agg att 402

Ile Phe Ala Leu Ser Leu Pro Phe Ser Gly Glu Arg Pro Arg Arg Ile

85

90

95

100

gac tgg atg gtt cct gag gct cac aga cag aac tgt agg aag aaa ggc 450

Asp Trp Met Val Pro Glu Ala His Arg Gln Asn Cys Arg Lys Lys Gly

105

110

115

aag aaa gag gac gaa tgt cac aat ttt gtc cag att ctc gcc att gcc 498

Lys Lys Glu Asp Glu Cys His Asn Phe Val Gln Ile Leu Ala Ile Ala

120

125

130

aat gcc tct cac ctc ctc act tgt ggc acc ttc gct ttt gat ccg aag 546

Asn Ala Ser His Leu Leu Thr Cys Gly Thr Phe Ala Phe Asp Pro Lys

135

140

145

tgc ggg gtt att gat gtg tcc agg ttc cag cag gtt gaa aga ctt gag 594

Cys Gly Val Ile Asp Val Ser Arg Phe Gln Gln Val Glu Arg Leu Glu

150

155

160

agt ggc cgg ggg aaa tgt cct ttt gag cca gct cag cgg tca gca gct 642

Ser Gly Arg Gly Lys Cys Pro Phe Glu Pro Ala Gln Arg Ser Ala Ala
165 170 175 180

gta atg gct ggg ggg gtc ctc tat gct gcc act gtg aaa aac tac ctg 690
Val Met Ala Gly Gly Val Leu Tyr Ala Ala Thr Val Lys Asn Tyr Leu
185 190 195

ggg acg gag cca att atc acc aga gca gtg ggt cgt gcc gag gac tgg 738
Gly Thr Glu Pro Ile Ile Thr Arg Ala Val Gly Arg Ala Glu Asp Trp
200 205 210

att cgg aca gat acc ttg cct tcc tgg ctg aac gcc cca gcc ttt gtc 786
Ile Arg Thr Asp Thr Leu Pro Ser Trp Leu Asn Ala Pro Ala Phe Val
215 220 225

gca gcc gtg gcc ttg agc cca gcc gaa tgg ggg gat gaa gat gga gac 834
Ala Ala Val Ala Leu Ser Pro Ala Glu Trp Gly Asp Glu Asp Gly Asp
230 235 240

gac gaa atc tac ttc ttc ttt acg gag act tcc cga gca ttt gac tca 882
Asp Glu Ile Tyr Phe Phe Phe Thr Glu Thr Ser Arg Ala Phe Asp Ser

245 250 255 260

tac gag cgc att aaa gtc cca cgg gtg gcc cgt gtg tgt gcg ggg gac 930
Tyr Glu Arg Ile Lys Val Pro Arg Val Ala Arg Val Cys Ala Gly Asp
265 270 275

ctc ggg ggc cgg aag acc ctc cag cag aga tgg acg acg ttt ttg aaa 978
Leu Gly Gly Arg Lys Thr Leu Gln Gln Arg Trp Thr Thr Phe Leu Lys

280

285

290

gct gac ctg ctc tgt cca ggg cct gag cat ggc cgg gcc tcc agt gtc 1026

Ala Asp Leu Leu Cys Pro Gly Pro Glu His Gly Arg Ala Ser Ser Val

295

300

305

ctg cag gat gtt gct gtg ctt cga cct gag ctt ggg gca ggg act ccc 1074

Leu Gln Asp Val Ala Val Leu Arg Pro Glu Leu Gly Ala Gly Thr Pro

310

315

320

atc ttt tat ggc atc ttt tct tcc cag tgg gag ggg gct act atc tct 1122

Ile Phe Tyr Gly Ile Phe Ser Ser Gln Trp Glu Gly Ala Thr Ile Ser

325

330

335

340

gct gtc tgt gcc ttc cga cca caa gac att cgg aca gtg ctg aat ggt 1170

Ala Val Cys Ala Phe Arg Pro Gln Asp Ile Arg Thr Val Leu Asn Gly

345

350

355

ccc ttc aga gaa cta aaa cat gac tgc aac aga gga ctg cct gtc gtg 1218

Pro Phe Arg Glu Leu Lys His Asp Cys Asn Arg Gly Leu Pro Val Val

360

365

370

gac aat gat gtg ccc cag ccc aga cct gga gag tgc atc acc aac aac 1266

Asp Asn Asp Val Pro Gln Pro Arg Pro Gly Glu Cys Ile Thr Asn Asn

375

380

385

atg aag ctc cgg cac ttt ggc tca tct ctc tcc ctg cct gac cgc gta 1314

Met Lys Leu Arg His Phe Gly Ser Ser Leu Ser Leu Pro Asp Arg Val

390

395

400

ctc acc ttc atc cgg gac cac cca ctc atg gac agg cca gtg ttt cca 1362
 Leu Thr Phe Ile Arg Asp His Pro Leu Met Asp Arg Pro Val Phe Pro
 405 410 415 420

gct gat ggc cac ccc ctg ctg gtc act aca gat aca gcc tat ctc aga 1410
 Ala Asp Gly His Pro Leu Leu Val Thr Thr Asp Thr Ala Tyr Leu Arg
 425 430 435

gtc gtg gcc cac agg gtg acc agc ctc tca ggg aaa gag tat gat gtg 1458
 Val Val Ala His Arg Val Thr Ser Leu Ser Gly Lys Glu Tyr Asp Val
 440 445 450

ctc tac ctg ggg aca gag gat gga cac ctc cac cga gca gtg cgg atc 1506
 Leu Tyr Leu Gly Thr Glu Asp Gly His Leu His Arg Ala Val Arg Ile
 455 460 465

gga gct cag ctc agc gtt ctt gaa gat ctg gcc tta ttc cca gag cca 1554
 Gly Ala Gln Leu Ser Val Leu Glu Asp Leu Ala Leu Phe Pro Glu Pro
 470 475 480

cag cca gtt gag aac atg aaa ttg tac cac agc tgg ctc ctg gtt ggc 1602
 Gln Pro Val Glu Asn Met Lys Leu Tyr His Ser Trp Leu Leu Val Gly
 485 490 495 500

tcc cgt act gag gtg aca caa gtg aat aca acc aac tgt ggc cgt ctc 1650
 Ser Arg Thr Glu Val Thr Gln Val Asn Thr Thr Asn Cys Gly Arg Leu
 505 510 515

cag agc tgc tca gag tgc atc ctg gcc cag gac cca gtc tgt gcc tgg 1698
Gln Ser Cys Ser Glu Cys Ile Leu Ala Gln Asp Pro Val Cys Ala Trp
520 525 530

agc ttc cgg ctg gat gag tgt gtg gcc cat gcc ggg gag cac cga ggg 1746
Ser Phe Arg Leu Asp Glu Cys Val Ala His Ala Gly Glu His Arg Gly
535 540 545

ttg gtc caa gac ata gag tca gca gat gtc tcc tct ttg tgt cct aaa 1794
Leu Val Gln Asp Ile Glu Ser Ala Asp Val Ser Ser Leu Cys Pro Lys
550 555 560

gag cct gga gaa cgt cca gta gtg ttt gaa gtt ccc gtg gct aca gct 1842
Glu Pro Gly Glu Arg Pro Val Val Phe Glu Val Pro Val Ala Thr Ala
565 570 575 580

gcg cat gtg gtc ttg cca tgt tct cca agc tca gca tgg gca tcc tgt 1890
Ala His Val Val Leu Pro Cys Ser Pro Ser Ser Ala Trp Ala Ser Cys
585 590 595

gtg tgg cac cag ccc agt gga gtg act gca ctc acc ccc cgg cgg gat 1938

Val Trp His Gln Pro Ser Gly Val Thr Ala Leu Thr Pro Arg Arg Asp
600 605 610

gga ctg gag gtg gtg gtg acc cca ggg gcc atg ggc gct tat gcc tgt 1986
Gly Leu Glu Val Val Val Thr Pro Gly Ala Met Gly Ala Tyr Ala Cys
615 620 625

gaa tgt cag gag ggt ggg gca gcc cat gtg gta gca gct tac agc ttg 2034

Glu Cys Gln Glu Gly Gly Ala Ala His Val Val Ala Ala Tyr Ser Leu

630

635

640

gta tgg ggc agc cag cga gat gct ccg agc cgg gcc cac aca gtg ggg 2082

Val Trp Gly Ser Gln Arg Asp Ala Pro Ser Arg Ala His Thr Val Gly

645

650

655

660

gcg gga ctg gct ggc ttc ttc ttg ggg att ctc gca gca tcc ctg act 2130

Ala Gly Leu Ala Gly Phe Phe Leu Gly Ile Leu Ala Ala Ser Leu Thr

665

670

675

ctc att ctg att ggt cgg cgt cag cag cga cgg cga cag agg gaa ctt 2178

Leu Ile Leu Ile Gly Arg Arg Gln Gln Arg Arg Arg Gln Arg Glu Leu

680

685

690

ctg gct aga gac aag gtg ggc ctg gac ctg ggg gct cca cct tct ggg 2226

Leu Ala Arg Asp Lys Val Gly Leu Asp Leu Gly Ala Pro Pro Ser Gly

695

700

705

acc aca agc tac agc caa gac cct ccc tcc ccc tct cct gaa gat gag 2274

Thr Thr Ser Tyr Ser Gln Asp Pro Pro Ser Pro Ser Pro Glu Asp Glu

710

715

720

cgg ttg ccg ctg gcc ctg gcc aag agg ggc agt ggc ttt ggt gga ttc 2322

Arg Leu Pro Leu Ala Leu Ala Lys Arg Gly Ser Gly Phe Gly Gly Phe

725

730

735

740

tca cca ccc ttc ctg ctt gat cct tgc cca agc cca gcc cac att cgg 2370

Ser Pro Pro Phe Leu Leu Asp Pro Cys Pro Ser Pro Ala His Ile Arg

745

750

755

cta act ggg gct cct cta gcc aca tgt gat gaa aca tcc atc 2412

Leu Thr Gly Ala Pro Leu Ala Thr Cys Asp Glu Thr Ser Ile

760

765

770

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gtgattactt ggattttagt atctgttctc tctgagcctg gatgggcttg gggccagacc 2592

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tgcttattct tcaagtttat ctgaatctgt ggggagtgc tgaatcccat gttgcaatat 2892

ggagtctctg ccctgagatc ttcccatct cagttttcct tccatgaaag agtacgtgta 2952

aatacatagt gttcataag 2971

<210> 66

<211> 770

<212> PRT

<213> Homo sapiens

<400> 66

Met Pro Ala Ser Ala Ala Arg Pro Arg Pro Gly Pro Gly Gln Pro Thr

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Ala Ser Pro Phe Pro Leu Leu Leu Ala Val Leu Ser Gly Pro Val

20 25 30

Ser Gly Arg Val Pro Arg Ser Val Pro Arg Thr Ser Leu Pro Ile Ser

35 40 45

Glu Ala Asp Ser Cys Leu Thr Arg Phe Ala Val Pro His Thr Tyr Asn

50 55 60

Tyr Ser Val Leu Leu Val Asp Pro Ala Ser His Thr Leu Tyr Val Gly

65 70 75 80

Ala Arg Asp Thr Ile Phe Ala Leu Ser Leu Pro Phe Ser Gly Glu Arg

85 90 95

Pro Arg Arg Ile Asp Trp Met Val Pro Glu Ala His Arg Gln Asn Cys

100 105 110

Arg Lys Lys Gly Lys Lys Glu Asp Glu Cys His Asn Phe Val Gln Ile

115 120 125

Leu Ala Ile Ala Asn Ala Ser His Leu Leu Thr Cys Gly Thr Phe Ala

130

135

140

Phe Asp Pro Lys Cys Gly Val Ile Asp Val Ser Arg Phe Gln Gln Val

145

150

155

160

Glu Arg Leu Glu Ser Gly Arg Gly Lys Cys Pro Phe Glu Pro Ala Gln

165

170

175

Arg Ser Ala Ala Val Met Ala Gly Gly Val Leu Tyr Ala Ala Thr Val

180

185

190

Lys Asn Tyr Leu Gly Thr Glu Pro Ile Ile Thr Arg Ala Val Gly Arg

195

200

205

Ala Glu Asp Trp Ile Arg Thr Asp Thr Leu Pro Ser Trp Leu Asn Ala

210

215

220

Pro Ala Phe Val Ala Ala Val Ala Leu Ser Pro Ala Glu Trp Gly Asp

225

230

235

240

Glu Asp Gly Asp Asp Glu Ile Tyr Phe Phe Phe Thr Glu Thr Ser Arg

245

250

255

Ala Phe Asp Ser Tyr Glu Arg Ile Lys Val Pro Arg Val Ala Arg Val

260

265

270

Cys Ala Gly Asp Leu Gly Gly Arg Lys Thr Leu Gln Gln Arg Trp Thr

275

280

285

Thr Phe Leu Lys Ala Asp Leu Leu Cys Pro Gly Pro Glu His Gly Arg
290 295 300

Ala Ser Ser Val Leu Gln Asp Val Ala Val Leu Arg Pro Glu Leu Gly
305 310 315 320

Ala Gly Thr Pro Ile Phe Tyr Gly Ile Phe Ser Ser Gln Trp Glu Gly
325 330 335

Ala Thr Ile Ser Ala Val Cys Ala Phe Arg Pro Gln Asp Ile Arg Thr
340 345 350

Val Leu Asn Gly Pro Phe Arg Glu Leu Lys His Asp Cys Asn Arg Gly
355 360 365

Leu Pro Val Val Asp Asn Asp Val Pro Gln Pro Arg Pro Gly Glu Cys
370 375 380

Ile Thr Asn Asn Met Lys Leu Arg His Phe Gly Ser Ser Leu Ser Leu
385 390 395 400

Pro Asp Arg Val Leu Thr Phe Ile Arg Asp His Pro Leu Met Asp Arg
405 410 415

Pro Val Phe Pro Ala Asp Gly His Pro Leu Leu Val Thr Thr Asp Thr
420 425 430

Ala Tyr Leu Arg Val Val Ala His Arg Val Thr Ser Leu Ser Gly Lys
435 440 445

Glu Tyr Asp Val Leu Tyr Leu Gly Thr Glu Asp Gly His Leu His Arg
450 455 460

Ala Val Arg Ile Gly Ala Gln Leu Ser Val Leu Glu Asp Leu Ala Leu
465 470 475 480

Phe Pro Glu Pro Gln Pro Val Glu Asn Met Lys Leu Tyr His Ser Trp
485 490 495

Leu Leu Val Gly Ser Arg Thr Glu Val Thr Gln Val Asn Thr Thr Asn
500 505 510

Cys Gly Arg Leu Gln Ser Cys Ser Glu Cys Ile Leu Ala Gln Asp Pro
515 520 525

Val Cys Ala Trp Ser Phe Arg Leu Asp Glu Cys Val Ala His Ala Gly
530 535 540

Glu His Arg Gly Leu Val Gln Asp Ile Glu Ser Ala Asp Val Ser Ser
545 550 555 560

Leu Cys Pro Lys Glu Pro Gly Glu Arg Pro Val Val Phe Glu Val Pro
565 570 575

Val Ala Thr Ala Ala His Val Val Leu Pro Cys Ser Pro Ser Ser Ala
580 585 590

Trp Ala Ser Cys Val Trp His Gln Pro Ser Gly Val Thr Ala Leu Thr

595

600

605

Pro Arg Arg Asp Gly Leu Glu Val Val Val Thr Pro Gly Ala Met Gly

610

615

620

Ala Tyr Ala Cys Glu Cys Gln Glu Gly Gly Ala Ala His Val Val Ala

625

630

635

640

Ala Tyr Ser Leu Val Trp Gly Ser Gln Arg Asp Ala Pro Ser Arg Ala

645

650

655

His Thr Val Gly Ala Gly Leu Ala Gly Phe Phe Leu Gly Ile Leu Ala

660

665

670

Ala Ser Leu Thr Leu Ile Leu Ile Gly Arg Arg Gln Gln Arg Arg Arg

675

680

685

Gln Arg Glu Leu Leu Ala Arg Asp Lys Val Gly Leu Asp Leu Gly Ala

690

695

700

Pro Pro Ser Gly Thr Thr Ser Tyr Ser Gln Asp Pro Pro Ser Pro Ser

705

710

715

720

Pro Glu Asp Glu Arg Leu Pro Leu Ala Leu Ala Lys Arg Gly Ser Gly

725

730

735

Phe Gly Gly Phe Ser Pro Pro Phe Leu Leu Asp Pro Cys Pro Ser Pro

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Ala His Ile Arg Leu Thr Gly Ala Pro Leu Ala Thr Cys Asp Glu Thr

755

760

765

Ser Ile

770

<210> 67

<211> 2244

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<213> Homo sapiens

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<221> CDS

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<400> 67

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gggaaatgca actcagctca ttgtccagc aggaattacc atg agc gga acg cag 175

Met Ser Gly Thr Gln

1

5

aca gga gtt gga ctt cca gta caa acg ctt cca gcc act caa gca tct 223

Thr Gly Val Gly Leu Pro Val Gln Thr Leu Pro Ala Thr Gln Ala Ser

10

15

20

cct gct gga caa tca tca tgt act act gct act ccc cca ttc aaa ggt 271

Pro Ala Gly Gln Ser Ser Cys Thr Thr Ala Thr Pro Pro Phe Lys Gly

25

30

35

gat aaa ata att tgc caa aag gag gag gaa gca aag gaa gca aca ggt 319

Asp Lys Ile Ile Cys Gln Lys Glu Glu Glu Ala Lys Glu Ala Thr Gly

40

45

50

tta cat gtt cat gaa cgt aaa att gaa gtc atg gag aac ccg tcc tgc 367

Leu His Val His Glu Arg Lys Ile Glu Val Met Glu Asn Pro Ser Cys

55

60

65

cga cga gga gcc aca aac acc agc aat ggg gat aca aag gaa aat gaa 415

Arg Arg Gly Ala Thr Asn Thr Ser Asn Gly Asp Thr Lys Glu Asn Glu

70

75

80

85

atg cat gtg gga agt ctt tta aat ggg aga aag tac agt gac tca agt 463

Met His Val Gly Ser Leu Leu Asn Gly Arg Lys Tyr Ser Asp Ser Ser

90

95

100

cta cct cct tca aac tca ggg aaa att caa agt gag act aat cag tgc 511

Leu Pro Pro Ser Asn Ser Gly Lys Ile Gln Ser Glu Thr Asn Gln Cys

105

110

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tca cta atc agt aat ggg cca tca ttg gaa tta ggt gag aat gga gca 559

Ser Leu Ile Ser Asn Gly Pro Ser Leu Glu Leu Gly Glu Asn Gly Ala

120

125

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tct ggg aaa cag aac tca gaa caa ata gac atg caa gat atc aaa agt 607

Ser Gly Lys Gln Asn Ser Glu Gln Ile Asp Met Gln Asp Ile Lys Ser
135 140 145

gat ttg aga aaa ccg cta gtt aat gga atc tgt gat ttt gat aaa gga 655
Asp Leu Arg Lys Pro Leu Val Asn Gly Ile Cys Asp Phe Asp Lys Gly
150 155 160 165

gat ggt tct cat tta agc aaa aac att cca aat cat aaa act tcc aat 703
Asp Gly Ser His Leu Ser Lys Asn Ile Pro Asn His Lys Thr Ser Asn
170 175 180

cat gta gga aat ggt gag ata tct cca atg gaa cca caa ggg act tta 751
His Val Gly Asn Gly Glu Ile Ser Pro Met Glu Pro Gln Gly Thr Leu
185 190 195

gat atc act cag caa gat act gcc aaa ggt gat caa cta gaa aga att 799
Asp Ile Thr Gln Gln Asp Thr Ala Lys Gly Asp Gln Leu Glu Arg Ile
200 205 210

tct aat gga cct gta tta act ttg ggt ggt tca tct gtg agc agt ata 847
Ser Asn Gly Pro Val Leu Thr Leu Gly Gly Ser Ser Val Ser Ser Ile

215 220 225

cag gag gct tca aat gcg gca aca cag caa ttt agt ggt act gat ttg 895
Gln Glu Ala Ser Asn Ala Ala Thr Gln Gln Phe Ser Gly Thr Asp Leu
230 235 240 245

ctt aat gga cct cta gct tca agt ttg aat tca gat gtg cct cag caa 943
Leu Asn Gly Pro Leu Ala Ser Ser Leu Asn Ser Asp Val Pro Gln Gln

250	255	260	
cgc cca agt gta gtt gtc tca cca cat tct aca acc tct gtt ata cag 991			
Arg Pro Ser Val Val Val Ser Pro His Ser Thr Thr Ser Val Ile Gln			
265	270	275	
gga cat caa atc ata gca gtt ccc gac tca gga tca aaa gta tcc cat 1039			
Gly His Gln Ile Ile Ala Val Pro Asp Ser Gly Ser Lys Val Ser His			
280	285	290	
tct cct gcc cta tca tct gac gtt cgg tct aca aat ggc aca gca gaa 1087			
Ser Pro Ala Leu Ser Ser Asp Val Arg Ser Thr Asn Gly Thr Ala Glu			
295	300	305	
tgc aaa act gta aag agg cca gca gag gat act gat agg gaa aca gtc 1135			
Cys Lys Thr Val Lys Arg Pro Ala Glu Asp Thr Asp Arg Glu Thr Val			
310	315	320	325
gca gga att cca aat aaa gta gga gtt aga att gtt aca atc agt gac 1183			
Ala Gly Ile Pro Asn Lys Val Gly Val Arg Ile Val Thr Ile Ser Asp			
330	335	340	
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ccc aac aat gct ggc tgc agc gca aca atg gtt gct gtg cca gca gga 1231			
Pro Asn Asn Ala Gly Cys Ser Ala Thr Met Val Ala Val Pro Ala Gly			
345	350	355	
gca gat cca agc act gta gct aaa gta gca ata gaa agt gct gtt cag 1279			
Ala Asp Pro Ser Thr Val Ala Lys Val Ala Ile Glu Ser Ala Val Gln			
360	365	370	

caa aag caa cag cat cca cca aca tat gta cag aat gtg gtc ccg cag 1327

Gln Lys Gln Gln His Pro Pro Thr Tyr Val Gln Asn Val Val Pro Gln

375

380

385

aac act cct atg cca cct tca cca gct gta caa gtg cag ggc cag cct 1375

Asn Thr Pro Met Pro Pro Ser Pro Ala Val Gln Val Gln Gly Gln Pro

390

395

400

405

aac agt tct cag cct tct cca ttc agt gga tcc agt cag cct gga gat 1423

Asn Ser Ser Gln Pro Ser Pro Phe Ser Gly Ser Ser Gln Pro Gly Asp

410

415

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cca atg aga aaa cct gga cag aac ttc atg tgt ctg tgg cag tct tgt 1471

Pro Met Arg Lys Pro Gly Gln Asn Phe Met Cys Leu Trp Gln Ser Cys

425

430

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aaa aag tgg ttt cag aca ccc tca cag gtt ttc tac cat gca gca act 1519

Lys Lys Trp Phe Gln Thr Pro Ser Gln Val Phe Tyr His Ala Ala Thr

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445

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gaa cat gga gga aaa gat gta tat cca ggg cag tgt ctt tgg gaa ggt 1567

Glu His Gly Gly Lys Asp Val Tyr Pro Gly Gln Cys Leu Trp Glu Gly

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460

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tgt gag cct ttt cag cga cag cgg ttt tct ttt att acc cac ttg cag 1615

Cys Glu Pro Phe Gln Arg Gln Arg Phe Ser Phe Ile Thr His Leu Gln

470

475

480

485

gat aag cac tgt tca aag gat gcc cta ctt gca gga tta aaa caa gat 1663

Asp Lys His Cys Ser Lys Asp Ala Leu Leu Ala Gly Leu Lys Gln Asp

490

495

500

gaa cca gga cac gca gga agt cag aag tct tct acc aag cag cca act 1711

Glu Pro Gly His Ala Gly Ser Gln Lys Ser Ser Thr Lys Gln Pro Thr

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510

515

gta ggg ggc aca agc tca act cct aga gca caa aag gcc att gtg aat 1759

Val Gly Gly Thr Ser Ser Thr Pro Arg Ala Gln Lys Ala Ile Val Asn

520

525

530

cat ccc agt gct gca ctt atg gct ctg agg aga gga tca aga aac ctt 1807

His Pro Ser Ala Ala Leu Met Ala Leu Arg Arg Gly Ser Arg Asn Leu

535

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gtc ttt cga gat ttt aca gat gaa aaa gag gga cca ata act aaa cac 1855

Val Phe Arg Asp Phe Thr Asp Glu Lys Glu Gly Pro Ile Thr Lys His

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atc cga cta aca gct gcc tta ata tta aaa aat att ggt aaa tat tca 1903

Ile Arg Leu Thr Ala Ala Leu Ile Leu Lys Asn Ile Gly Lys Tyr Ser

570

575

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gaa tgt ggt cgc aga ttg tta aag aga cat gaa aat aac tta tca gtg 1951

Glu Cys Gly Arg Arg Leu Leu Lys Arg His Glu Asn Asn Leu Ser Val

585

590

595

cta gcc att agt aac atg gaa gct tcc tcc acc ctt gcc aaa tgc ctt 1999

Leu Ala Ile Ser Asn Met Glu Ala Ser Ser Thr Leu Ala Lys Cys Leu

600

605

610

tat gaa ctt aat ttt aca gtt cag agt aag gaa caa gaa aaa gac tca 2047

Tyr Glu Leu Asn Phe Thr Val Gln Ser Lys Glu Gln Glu Lys Asp Ser

615

620

625

gaa atg ctg cag tgaaaaataa ttccacttac acagtggggg actcaaagtc 2099

Glu Met Leu Gln

630

agccacattt cacatactgt tactgaagaa agcaccaagt cttaatggaa caaagacat 2159

agaatgaatt attttatctc ctcccatgat gctgagagga agcttcgtat tctgatctct 2219

gagtgaatcc ctttgttctc tgttt 2244

<210> 68

<211> 633

<212> PRT

<213> Homo sapiens

<400> 68

Met Ser Gly Thr Gln Thr Gly Val Gly Leu Pro Val Gln Thr Leu Pro

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Ala Thr Gln Ala Ser Pro Ala Gly Gln Ser Ser Cys Thr Thr Ala Thr

20

25

30

Pro Pro Phe Lys Gly Asp Lys Ile Ile Cys Gln Lys Glu Glu Glu Ala

35

40

45

Lys Glu Ala Thr Gly Leu His Val His Glu Arg Lys Ile Glu Val Met

50

55

60

Glu Asn Pro Ser Cys Arg Arg Gly Ala Thr Asn Thr Ser Asn Gly Asp

65

70

75

80

Thr Lys Glu Asn Glu Met His Val Gly Ser Leu Leu Asn Gly Arg Lys

85

90

95

Tyr Ser Asp Ser Ser Leu Pro Pro Ser Asn Ser Gly Lys Ile Gln Ser

100

105

110

Glu Thr Asn Gln Cys Ser Leu Ile Ser Asn Gly Pro Ser Leu Glu Leu

115

120

125

Gly Glu Asn Gly Ala Ser Gly Lys Gln Asn Ser Glu Gln Ile Asp Met

130

135

140

Gln Asp Ile Lys Ser Asp Leu Arg Lys Pro Leu Val Asn Gly Ile Cys

145

150

155

160

Asp Phe Asp Lys Gly Asp Gly Ser His Leu Ser Lys Asn Ile Pro Asn

165

170

175

His Lys Thr Ser Asn His Val Gly Asn Gly Glu Ile Ser Pro Met Glu

180

185

190

Pro Gln Gly Thr Leu Asp Ile Thr Gln Gln Asp Thr Ala Lys Gly Asp

195

200

205

Gln Leu Glu Arg Ile Ser Asn Gly Pro Val Leu Thr Leu Gly Gly Ser

210

215

220

Ser Val Ser Ser Ile Gln Glu Ala Ser Asn Ala Ala Thr Gln Gln Phe

225

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240

Ser Gly Thr Asp Leu Leu Asn Gly Pro Leu Ala Ser Ser Leu Asn Ser

245

250

255

Asp Val Pro Gln Gln Arg Pro Ser Val Val Val Ser Pro His Ser Thr

260

265

270

Thr Ser Val Ile Gln Gly His Gln Ile Ile Ala Val Pro Asp Ser Gly

275

280

285

Ser Lys Val Ser His Ser Pro Ala Leu Ser Ser Asp Val Arg Ser Thr

290

295

300

Asn Gly Thr Ala Glu Cys Lys Thr Val Lys Arg Pro Ala Glu Asp Thr

305

310

315

320

Asp Arg Glu Thr Val Ala Gly Ile Pro Asn Lys Val Gly Val Arg Ile

325

330

335

Val Thr Ile Ser Asp Pro Asn Asn Ala Gly Cys Ser Ala Thr Met Val
340 345 350

Ala Val Pro Ala Gly Ala Asp Pro Ser Thr Val Ala Lys Val Ala Ile
355 360 365

Glu Ser Ala Val Gln Gln Lys Gln Gln His Pro Pro Thr Tyr Val Gln
370 375 380

Asn Val Val Pro Gln Asn Thr Pro Met Pro Pro Ser Pro Ala Val Gln
385 390 395 400

Val Gln Gly Gln Pro Asn Ser Ser Gln Pro Ser Pro Phe Ser Gly Ser
405 410 415

Ser Gln Pro Gly Asp Pro Met Arg Lys Pro Gly Gln Asn Phe Met Cys
420 425 430

Leu Trp Gln Ser Cys Lys Lys Trp Phe Gln Thr Pro Ser Gln Val Phe
435 440 445

Tyr His Ala Ala Thr Glu His Gly Gly Lys Asp Val Tyr Pro Gly Gln
450 455 460

Cys Leu Trp Glu Gly Cys Glu Pro Phe Gln Arg Gln Arg Phe Ser Phe
465 470 475 480

Ile Thr His Leu Gln Asp Lys His Cys Ser Lys Asp Ala Leu Leu Ala
485 490 495

Gly Leu Lys Gln Asp Glu Pro Gly His Ala Gly Ser Gln Lys Ser Ser

500

505

510

Thr Lys Gln Pro Thr Val Gly Gly Thr Ser Ser Thr Pro Arg Ala Gln

515

520

525

Lys Ala Ile Val Asn His Pro Ser Ala Ala Leu Met Ala Leu Arg Arg

530

535

540

Gly Ser Arg Asn Leu Val Phe Arg Asp Phe Thr Asp Glu Lys Glu Gly

545

550

555

560

Pro Ile Thr Lys His Ile Arg Leu Thr Ala Ala Leu Ile Leu Lys Asn

565

570

575

Ile Gly Lys Tyr Ser Glu Cys Gly Arg Arg Leu Leu Lys Arg His Glu

580

585

590

Asn Asn Leu Ser Val Leu Ala Ile Ser Asn Met Glu Ala Ser Ser Thr

595

600

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Leu Ala Lys Cys Leu Tyr Glu Leu Asn Phe Thr Val Gln Ser Lys Glu

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Gln Glu Lys Asp Ser Glu Met Leu Gln

625

630

<210> 69

<211> 3253

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (9)..(2588)

<400> 69

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Met Ala Pro Ala Gly Cys Cys Cys Cys Cys Cys Phe Trp Gly

1

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10

ggc gct gtg gcc gcc gcg ggc gcc gcc cgg cgt gtc ctg ctg ctg ctg 98

Gly Ala Val Ala Ala Ala Gly Ala Ala Arg Arg Val Leu Leu Leu Leu

15

20

25

30

ctg ctg ggg gtc ctg tcc gct ggg ctg cgg cca ggc gcc ctg gcc acc 146

Leu Leu Gly Val Leu Ser Ala Gly Leu Arg Pro Gly Ala Leu Ala Thr

35

40

45

gag cac tac tcg ccg ctc tcc ctg ctc aag cag gag ctg cag cac cgg 194

Glu His Tyr Ser Pro Leu Ser Leu Leu Lys Gln Glu Leu Gln His Arg

50

55

60

cag cag cag gag gcc ccg gcg ggc ggc ggc ggc tgc agc ccg cag tcc 242

Gln Gln Gln Glu Ala Pro Ala Gly Gly Gly Gly Cys Ser Pro Gln Ser

65

70

75

ggg gac tgg ggg gac cag tac tct gcc gag tgc ggc gag tca tcc ttt 290
Gly Asp Trp Gly Asp Gln Tyr Ser Ala Glu Cys Gly Glu Ser Ser Phe
80 85 90

ttg aac ttc cat gac tca gac tgc gaa ccc aag gga tca tca ccc tgt 338
Leu Asn Phe His Asp Ser Asp Cys Glu Pro Lys Gly Ser Ser Pro Cys
95 100 105 110

gac tcc ttg ctt tcc ctc aac act gag aag att ctg agc cag gcc aag 386
Asp Ser Leu Leu Ser Leu Asn Thr Glu Lys Ile Leu Ser Gln Ala Lys
115 120 125

tct att gca gaa cag aag aga ttc ccg ttt gcc act gat aat gac agc 434
Ser Ile Ala Glu Gln Lys Arg Phe Pro Phe Ala Thr Asp Asn Asp Ser
130 135 140

aca aat gaa gag tta gct att gct tat gtc ttg att ggc agt ggt ctg 482
Thr Asn Glu Glu Leu Ala Ile Ala Tyr Val Leu Ile Gly Ser Gly Leu
145 150 155

tat gat gaa gca ata cgg cat ttt tca aca atg ctt cag gag gag cct 530
Tyr Asp Glu Ala Ile Arg His Phe Ser Thr Met Leu Gln Glu Glu Pro
160 165 170

gat ctg gtt agt gca att tat ggc cga ggg ata gcc tat gga aag aag 578
Asp Leu Val Ser Ala Ile Tyr Gly Arg Gly Ile Ala Tyr Gly Lys Lys
175 180 185 190

gga cta cat gac att aag aat gct gag ctt gct ctg ttc gaa ctg agc 626
Gly Leu His Asp Ile Lys Asn Ala Glu Leu Ala Leu Phe Glu Leu Ser
195 200 205

cga gta att acc ttg gaa cca gat cgt cca gag gta ttt gag cag cga 674
Arg Val Ile Thr Leu Glu Pro Asp Arg Pro Glu Val Phe Glu Gln Arg
210 215 220

gca gaa att ctg tcc cct ctg gga cga att aat gaa gca gtg aat gac 722
Ala Glu Ile Leu Ser Pro Leu Gly Arg Ile Asn Glu Ala Val Asn Asp
225 230 235

ctc act aaa gct atc caa ctg cag ccc tca gca cgg ctg tac aga cat 770
Leu Thr Lys Ala Ile Gln Leu Gln Pro Ser Ala Arg Leu Tyr Arg His
240 245 250

cgg gga acc ctg tac ttc ata tca gag gac tat gca aca gcc cat gaa 818
Arg Gly Thr Leu Tyr Phe Ile Ser Glu Asp Tyr Ala Thr Ala His Glu
255 260 265 270

gac ttt cag cag tcc tta gaa ctg aac aaa aac cag cct ata gct atg 866
Asp Phe Gln Gln Ser Leu Glu Leu Asn Lys Asn Gln Pro Ile Ala Met
275 280 285

cta tac aaa ggt tta act ttc ttt cac aga gga ctt ctg aag gaa gct 914
Leu Tyr Lys Gly Leu Thr Phe Phe His Arg Gly Leu Leu Lys Glu Ala
290 295 300

att gaa tcc ttc aaa gaa gct ttg aag cag aaa gtt gac ttt att gat 962

Ile Glu Ser Phe Lys Glu Ala Leu Lys Gln Lys Val Asp Phe Ile Asp
 305 310 315

gca tat aaa agt. cta ggg cag gca tat aga gaa ctg ggc aat ttt gaa 1010
 Ala Tyr Lys Ser Leu Gly Gln Ala Tyr Arg Glu Leu Gly Asn Phe Glu
 320 325 330

gca gcc act gag agc ttt caa aag gca ctg ttg ctc aac caa aat cat 1058
 Ala Ala Thr Glu Ser Phe Gln Lys Ala Leu Leu Leu Asn Gln Asn His
 335 340 345 350

gtg caa acc ctc cag ctc cgg gga atg atg ctc tac cac cac ggc agc 1106
 Val Gln Thr Leu Gln Leu Arg Gly Met Met Leu Tyr His His Gly Ser
 355 360 365

tta cag gaa gcc ctt aag aac ttt aag cgg tgt ctg cag cta gag cca 1154
 Leu Gln Glu Ala Leu Lys Asn Phe Lys Arg Cys Leu Gln Leu Glu Pro
 370 375 380

tat aat gaa gtg tgc cag tat atg aaa ggg ctc agc cat gtt gcc atg 1202
 Tyr Asn Glu Val Cys Gln Tyr Met Lys Gly Leu Ser His Val Ala Met
 385 390 395

gga cag ttt tat gaa ggg ata aaa gca caa aca aaa gtt atg ctg aat 1250
 Gly Gln Phe Tyr Glu Gly Ile Lys Ala Gln Thr Lys Val Met Leu Asn
 400 405 410

gat cct ctc cca ggc cag aag gct agc cct gag tat ctt aaa gta aag 1298
 Asp Pro Leu Pro Gly Gln Lys Ala Ser Pro Glu Tyr Leu Lys Val Lys

415

420

425

430

tat ctc cga gag tac tct cga cat ctt cat gca cac ctt gat acc ccc 1346

Tyr Leu Arg Glu Tyr Ser Arg His Leu His Ala His Leu Asp Thr Pro

435

440

445

ctt acg gaa tat aac att gat gtg gat ctg cct gga agc ttt aag gac 1394

Leu Thr Glu Tyr Asn Ile Asp Val Asp Leu Pro Gly Ser Phe Lys Asp

450

455

460

cac tgg gct aaa aat ttg cct ttc ctc ata gaa gac tac gaa gag cag 1442

His Trp Ala Lys Asn Leu Pro Phe Leu Ile Glu Asp Tyr Glu Glu Gln

465

470

475

cca ggg ttg caa ccc cac ata aaa gat gtg tta cat cag aat ttt gag 1490

Pro Gly Leu Gln Pro His Ile Lys Asp Val Leu His Gln Asn Phe Glu

480

485

490

agt tat aag cct gaa gta cag gag ctg att tgt gtg gct gat cgt ttg 1538

Ser Tyr Lys Pro Glu Val Gln Glu Leu Ile Cys Val Ala Asp Arg Leu

495

500

505

510

gga tcc ctg atg caa tat gaa aca cct ggt ttc ctg cca aac aag aga 1586

Gly Ser Leu Met Gln Tyr Glu Thr Pro Gly Phe Leu Pro Asn Lys Arg

515

520

525

ata cac aga gct atg ggt ttg gcc gca ttg gag gtc atg caa gcc gtg 1634

Ile His Arg Ala Met Gly Leu Ala Ala Leu Glu Val Met Gln Ala Val

530

535

540

cag cgt aca tgg acc aac tcg aaa gtt cga atg aat ggg aag aca cgg 1682

Gln Arg Thr Trp Thr Asn Ser Lys Val Arg Met Asn Gly Lys Thr Arg

545

550

555

ttg atg cag tgg aga gac atg ttt gac att gca gtt aaa tgg aga agg 1730

Leu Met Gln Trp Arg Asp Met Phe Asp Ile Ala Val Lys Trp Arg Arg

560

565

570

att gct gac cca gac cag ccc gtg ctg tgg tta gat caa atg cca gca 1778

Ile Ala Asp Pro Asp Gln Pro Val Leu Trp Leu Asp Gln Met Pro Ala

575

580

585

590

cga agt ctt agc aga ggt ttt aac aac cac att aat tta atc agg ggt 1826

Arg Ser Leu Ser Arg Gly Phe Asn Asn His Ile Asn Leu Ile Arg Gly

595

600

605

cag gtg atc aac atg aga tac cta gaa tat ttt gag aaa ata ctt cat 1874

Gln Val Ile Asn Met Arg Tyr Leu Glu Tyr Phe Glu Lys Ile Leu His

610

615

620

ttt att aaa gac aga att ctt gtt tat cat gga gct aat aat cct aaa 1922

Phe Ile Lys Asp Arg Ile Leu Val Tyr His Gly Ala Asn Asn Pro Lys

625

630

635

gga ttg ctg gaa gtt cgg gaa gcc ctg gaa aag gta cac aaa gta gaa 1970

Gly Leu Leu Glu Val Arg Glu Ala Leu Glu Lys Val His Lys Val Glu

640

645

650

gac ctt ctt ccg att atg aag cag ttt aat act aaa acg aag gat ggg 2018
Asp Leu Leu Pro Ile Met Lys Gln Phe Asn Thr Lys Thr Lys Asp Gly
655 660 665 670

ttc acc gtg aac aca aaa gtt ccc agc ctt aaa gac caa ggg aag gaa 2066
Phe Thr Val Asn Thr Lys Val Pro Ser Leu Lys Asp Gln Gly Lys Glu
675 680 685

tat gat gga ttc aca atc acg att aca gga gac aaa gtt ggc aat ata 2114
Tyr Asp Gly Phe Thr Ile Thr Ile Thr Gly Asp Lys Val Gly Asn Ile
690 695 700

tta ttt tct gtg gaa act caa acc acg gaa gaa agg aca caa tta tat 2162
Leu Phe Ser Val Glu Thr Gln Thr Thr Glu Glu Arg Thr Gln Leu Tyr
705 710 715

cat gct gaa ata gat gca ctt tat aaa gat ttg aca gca aaa gga aaa 2210
His Ala Glu Ile Asp Ala Leu Tyr Lys Asp Leu Thr Ala Lys Gly Lys
720 725 730

gta ttg att ctt tca tca gaa ttt ggg gag gct gat gct gtc tgc aac 2258
Val Leu Ile Leu Ser Ser Glu Phe Gly Glu Ala Asp Ala Val Cys Asn
735 740 745 750

tta atc tta tcc tta gtt tat tac ttt tat aat tta atg cca ctc tct 2306
Leu Ile Leu Ser Leu Val Tyr Tyr Phe Tyr Asn Leu Met Pro Leu Ser
755 760 765

cga gga tcc agt gta att gct tac tcg gtc atc gtg gga gca ctg atg 2354

Arg Gly Ser Ser Val Ile Ala Tyr Ser Val Ile Val Gly Ala Leu Met

770

775

780

gca agt gga aaa gaa gta gca gga aaa att ccc aaa ggg aag tta gtc 2402

Ala Ser Gly Lys Glu Val Ala Gly Lys Ile Pro Lys Gly Lys Leu Val

785

790

795

gac ttt gaa gct atg aca gcc cct ggt tca gag gcc ttt agc aaa gtc 2450

Asp Phe Glu Ala Met Thr Ala Pro Gly Ser Glu Ala Phe Ser Lys Val

800

805

810

gcc aaa agc tgg atg aac ttg aaa agt att tca cct tct tat aag act 2498

Ala Lys Ser Trp Met Asn Leu Lys Ser Ile Ser Pro Ser Tyr Lys Thr

815

820

825

830

ctt cca tca gtt tca gaa acg ttt cca acg tta aga tcg atg att gag 2546

Leu Pro Ser Val Ser Glu Thr Phe Pro Thr Leu Arg Ser Met Ile Glu

835

840

845

gtg cta aac aca gac tct tct cca cgt tgt ctt aag aaa ctc 2588

Val Leu Asn Thr Asp Ser Ser Pro Arg Cys Leu Lys Lys Leu

850

855

860

tagttctgct gctgtattta tacaagtaaa gggccggacc tcttgcttct taagttattt 2648

tttaaaacat ggaattataa agaaattagg tcctctatta ctttgatac caatttttat 2708

aggaattgaa tacttgaaat cattttcttt acttttctga accataatga aaatcatgaa 2768

agaggctttc ggggggaaaa agctacttga cttggaggga aagcgtatgt attagccggc 2828

agcctgttgg ttcccactta taaagtcata taactccttc cttacagtaa aaaaaatttt 2888

cctcaacaac taaaatataa tactgaagat gaacaaaaac aaaaccaa at aggagtgttt 2948

gtattccttt agagatctgg atatttttca aagacttgct ttttacgcac attgtgatag 3008

agcatctttt gttgactcac gtaacctcca tgtgtgggic cttgttttta ttagaacct 3068

ggaagaaggt tcctgggcca tcagtatgtg ttgcagagct cacagccagg aacacttatt 3128

ttgaacaatg cagacagtac ttgccagagt cccaaatgct gaattattga accatgtttt 3188

tttttccctt tgttgaaaaa aataaaccag ggtgatttct ataaatcacc agtttttggc 3248

attgg 3253

<210> 70

<211> 860

<212> PRT

<213> Homo sapiens

<400> 70

Met Ala Pro Ala Gly Cys Cys Cys Cys Cys Cys Phe Trp Gly Gly Ala

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Val Ala Ala Ala Gly Ala Ala Arg Arg Val Leu Leu Leu Leu Leu Leu

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Gly Val Leu Ser Ala Gly Leu Arg Pro Gly Ala Leu Ala Thr Glu His

35

40

45

Tyr Ser Pro Leu Ser Leu Leu Lys Gln Glu Leu Gln His Arg Gln Gln

50

55

60

Gln Glu Ala Pro Ala Gly Gly Gly Gly Cys Ser Pro Gln Ser Gly Asp

65

70

75

80

Trp Gly Asp Gln Tyr Ser Ala Glu Cys Gly Glu Ser Ser Phe Leu Asn

85

90

95

Phe His Asp Ser Asp Cys Glu Pro Lys Gly Ser Ser Pro Cys Asp Ser

100

105

110

Leu Leu Ser Leu Asn Thr Glu Lys Ile Leu Ser Gln Ala Lys Ser Ile

115

120

125

Ala Glu Gln Lys Arg Phe Pro Phe Ala Thr Asp Asn Asp Ser Thr Asn

130

135

140

Glu Glu Leu Ala Ile Ala Tyr Val Leu Ile Gly Ser Gly Leu Tyr Asp

145

150

155

160

Glu Ala Ile Arg His Phe Ser Thr Met Leu Gln Glu Glu Pro Asp Leu

165

170

175

Val Ser Ala Ile Tyr Gly Arg Gly Ile Ala Tyr Gly Lys Lys Gly Leu

180

185

190

His Asp Ile Lys Asn Ala Glu Leu Ala Leu Phe Glu Leu Ser Arg Val

195

200

205

Ile Thr Leu Glu Pro Asp Arg Pro Glu Val Phe Glu Gln Arg Ala Glu

210

215

220

Ile Leu Ser Pro Leu Gly Arg Ile Asn Glu Ala Val Asn Asp Leu Thr

225

230

235

240

Lys Ala Ile Gln Leu Gln Pro Ser Ala Arg Leu Tyr Arg His Arg Gly

245

250

255

Thr Leu Tyr Phe Ile Ser Glu Asp Tyr Ala Thr Ala His Glu Asp Phe

260

265

270

Gln Gln Ser Leu Glu Leu Asn Lys Asn Gln Pro Ile Ala Met Leu Tyr

275

280

285

Lys Gly Leu Thr Phe Phe His Arg Gly Leu Leu Lys Glu Ala Ile Glu

290

295

300

Ser Phe Lys Glu Ala Leu Lys Gln Lys Val Asp Phe Ile Asp Ala Tyr

305

310

315

320

Lys Ser Leu Gly Gln Ala Tyr Arg Glu Leu Gly Asn Phe Glu Ala Ala

325

330

335

Thr Glu Ser Phe Gln Lys Ala Leu Leu Leu Asn Gln Asn His Val Gln

340

345

350

Thr Leu Gln Leu Arg Gly Met Met Leu Tyr His His Gly Ser Leu Gln

355

360

365

Glu Ala Leu Lys Asn Phe Lys Arg Cys Leu Gln Leu Glu Pro Tyr Asn

370

375

380

Glu Val Cys Gln Tyr Met Lys Gly Leu Ser His Val Ala Met Gly Gln

385

390

395

400

Phe Tyr Glu Gly Ile Lys Ala Gln Thr Lys Val Met Leu Asn Asp Pro

405

410

415

Leu Pro Gly Gln Lys Ala Ser Pro Glu Tyr Leu Lys Val Lys Tyr Leu

420

425

430

Arg Glu Tyr Ser Arg His Leu His Ala His Leu Asp Thr Pro Leu Thr

435

440

445

Glu Tyr Asn Ile Asp Val Asp Leu Pro Gly Ser Phe Lys Asp His Trp

450

455

460

Ala Lys Asn Leu Pro Phe Leu Ile Glu Asp Tyr Glu Glu Gln Pro Gly

465

470

475

480

Leu Gln Pro His Ile Lys Asp Val Leu His Gln Asn Phe Glu Ser Tyr

485

490

495

Lys Pro Glu Val Gln Glu Leu Ile Cys Val Ala Asp Arg Leu Gly Ser

500

505

510

Leu Met Gln Tyr Glu Thr Pro Gly Phe Leu Pro Asn Lys Arg Ile His

515

520

525

Arg Ala Met Gly Leu Ala Ala Leu Glu Val Met Gln Ala Val Gln Arg

530

535

540

Thr Trp Thr Asn Ser Lys Val Arg Met Asn Gly Lys Thr Arg Leu Met

545

550

555

560

Gln Trp Arg Asp Met Phe Asp Ile Ala Val Lys Trp Arg Arg Ile Ala

565

570

575

Asp Pro Asp Gln Pro Val Leu Trp Leu Asp Gln Met Pro Ala Arg Ser

580

585

590

Leu Ser Arg Gly Phe Asn Asn His Ile Asn Leu Ile Arg Gly Gln Val

595

600

605

Ile Asn Met Arg Tyr Leu Glu Tyr Phe Glu Lys Ile Leu His Phe Ile

610

615

620

Lys Asp Arg Ile Leu Val Tyr His Gly Ala Asn Asn Pro Lys Gly Leu

625

630

635

640

Leu Glu Val Arg Glu Ala Leu Glu Lys Val His Lys Val Glu Asp Leu
645 650 655

Leu Pro Ile Met Lys Gln Phe Asn Thr Lys Thr Lys Asp Gly Phe Thr
660 665 670

Val Asn Thr Lys Val Pro Ser Leu Lys Asp Gln Gly Lys Glu Tyr Asp
675 680 685

Gly Phe Thr Ile Thr Ile Thr Gly Asp Lys Val Gly Asn Ile Leu Phe
690 695 700

Ser Val Glu Thr Gln Thr Thr Glu Glu Arg Thr Gln Leu Tyr His Ala
705 710 715 720

Glu Ile Asp Ala Leu Tyr Lys Asp Leu Thr Ala Lys Gly Lys Val Leu
725 730 735

Ile Leu Ser Ser Glu Phe Gly Glu Ala Asp Ala Val Cys Asn Leu Ile
740 745 750

Leu Ser Leu Val Tyr Tyr Phe Tyr Asn Leu Met Pro Leu Ser Arg Gly
755 760 765

Ser Ser Val Ile Ala Tyr Ser Val Ile Val Gly Ala Leu Met Ala Ser
770 775 780

Gly Lys Glu Val Ala Gly Lys Ile Pro Lys Gly Lys Leu Val Asp Phe
785 790 795 800

Glu Ala Met Thr Ala Pro Gly Ser Glu Ala Phe Ser Lys Val Ala Lys

805

810

815

Ser Trp Met Asn Leu Lys Ser Ile Ser Pro Ser Tyr Lys Thr Leu Pro

820

825

830

Ser Val Ser Glu Thr Phe Pro Thr Leu Arg Ser Met Ile Glu Val Leu

835

840

845

Asn Thr Asp Ser Ser Pro Arg Cys Leu Lys Lys Leu

850

855

860

<210> 71

<211> 2195

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (266)..(1714)

<400> 71

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gacgcagggc gctgggccgg gtttcggctt cggccacagg agtcatagag gctgggtggt 180

ctggcaagga cttgtgcatt tgagaactga caggtgcagc ggagacttct aagaggga 240

accaagcttt ttttctcaag gtgca atg aaa gcc ttc cac act ttc tgt gtt 292

Met Lys Ala Phe His Thr Phe Cys Val

1

5

gtc ctt ctg gtg ttt ggg agt gtc tct gaa gcc aag ttt gat gat ttt 340

Val Leu Leu Val Phe Gly Ser Val Ser Glu Ala Lys Phe Asp Asp Phe

10

15

20

25

gag gat gag gag gac ata gta gag tat gat gat aat gac ttc gct gaa 388

Glu Asp Glu Glu Asp Ile Val Glu Tyr Asp Asp Asn Asp Phe Ala Glu

30

35

40

ttt gag gat gtc atg gaa gac tct gtt act gaa tct cct caa cgg gtc 436

Phe Glu Asp Val Met Glu Asp Ser Val Thr Glu Ser Pro Gln Arg Val

45

50

55

ata atc act gaa gat gat gaa gat gag acc act gtg gag ttg gaa ggg 484

Ile Ile Thr Glu Asp Asp Glu Asp Glu Thr Thr Val Glu Leu Glu Gly

60

65

70

cag gat gaa aac caa gaa gga gat ttt gaa gat gca gat acc cag gag 532

Gln Asp Glu Asn Gln Glu Gly Asp Phe Glu Asp Ala Asp Thr Gln Glu

75

80

85

gga gat act gag agt gaa cca tat gat gat gaa gaa ttt gaa ggt tat 580

Gly Asp Thr Glu Ser Glu Pro Tyr Asp Asp Glu Glu Phe Glu Gly Tyr

90	95	100	105
gaa gac aaa cca gat act tct tct agc aaa aat aaa gac cca ata acg 628			
Glu Asp Lys Pro Asp Thr Ser Ser Ser Lys Asn Lys Asp Pro Ile Thr			
110	115	120	
att gtt gat gtt cct gca cac ctc cag aac agc tgg gag agt tat tat 676			
Ile Val Asp Val Pro Ala His Leu Gln Asn Ser Trp Glu Ser Tyr Tyr			
125	130	135	
cta gaa att ttg atg gtg act ggt ctg ctt gct tat atc atg aat tac 724			
Leu Glu Ile Leu Met Val Thr Gly Leu Leu Ala Tyr Ile Met Asn Tyr			
140	145	150	
atc att ggg aag aat aaa aac agt cgc ctt gca cag gcc tgg ttt aac 772			
Ile Ile Gly Lys Asn Lys Asn Ser Arg Leu Ala Gln Ala Trp Phe Asn			
155	160	165	
act cat agg gag ctt ttg gag agc aac ttt act tta gtg ggg gat gat 820			
Thr His Arg Glu Leu Leu Glu Ser Asn Phe Thr Leu Val Gly Asp Asp			
170	175	180	185
gga act aac aaa gaa gcc aca agc aca gga aag ttg aac cag gag aat 868			
Gly Thr Asn Lys Glu Ala Thr Ser Thr Gly Lys Leu Asn Gln Glu Asn			
190	195	200	
gag cac atc tat aac ctg tgg tgt tct ggt cga gtg tgc tgt gag ggc 916			
Glu His Ile Tyr Asn Leu Trp Cys Ser Gly Arg Val Cys Cys Glu Gly			
205	210	215	

atg ctt atc cag ctg agg ttc ctc aag aga caa gac tta ctg aat gtc 964

Met Leu Ile Gln Leu Arg Phe Leu Lys Arg Gln Asp Leu Leu Asn Val

220

225

230

ctg gcc cgg atg atg agg cca gtg agt gat caa gtg caa ata aaa gta 1012

Leu Ala Arg Met Met Arg Pro Val Ser Asp Gln Val Gln Ile Lys Val

235

240

245

acc atg aat gat gaa gac atg gat acc tac gta ttt gct gtt ggc aca 1060

Thr Met Asn Asp Glu Asp Met Asp Thr Tyr Val Phe Ala Val Gly Thr

250

255

260

265

cgg aaa gcc ttg gtg cga cta cag aaa gag atg cag gat ttg agt gag 1108

Arg Lys Ala Leu Val Arg Leu Gln Lys Glu Met Gln Asp Leu Ser Glu

270

275

280

ttt tgt agt gat aaa cct aag tct gga gca aag tat gga ctg ccg gac 1156

Phe Cys Ser Asp Lys Pro Lys Ser Gly Ala Lys Tyr Gly Leu Pro Asp

285

290

295

tct ttg gcc atc ctg tca gag atg gga gaa gtc aca gac gga atg atg 1204

Ser Leu Ala Ile Leu Ser Glu Met Gly Glu Val Thr Asp Gly Met Met

300

305

310

gat aca aag atg gtt cac ttt ctt aca cac tat gct gac aag att gaa 1252

Asp Thr Lys Met Val His Phe Leu Thr His Tyr Ala Asp Lys Ile Glu

315

320

325

tct gtt cat ttt tca gac cag ttc tct ggt cca aaa att atg caa gag 1300

Ser Val His Phe Ser Asp Gln Phe Ser Gly Pro Lys Ile Met Gln Glu

330 335 340 345

gaa ggt cag cct tta aag cta cct gac act aag agg aca ctg ttg ttt 1348

Glu Gly Gln Pro Leu Lys Leu Pro Asp Thr Lys Arg Thr Leu Leu Phe

350 355 360

aca ttt aat gtg cct ggc tca ggt aac act tac cca aag gat atg gag 1396

Thr Phe Asn Val Pro Gly Ser Gly Asn Thr Tyr Pro Lys Asp Met Glu

365 370 375

gca ctg cta ccc ctg atg aac atg gtg att tat tct att gat aaa gcc 1444

Ala Leu Leu Pro Leu Met Asn Met Val Ile Tyr Ser Ile Asp Lys Ala

380 385 390

aaa aag ttc cga ctc aac aga gaa ggc aaa caa aaa gca gat aag aac 1492

Lys Lys Phe Arg Leu Asn Arg Glu Gly Lys Gln Lys Ala Asp Lys Asn

395 400 405

cgt gcc cga gta gaa gag aac ttc ttg aaa ctg aca cat gtg caa aga 1540

Arg Ala Arg Val Glu Glu Asn Phe Leu Lys Leu Thr His Val Gln Arg

410 415 420 425

cag gaa gca gca cag tct cgg cgg gag gag aaa aaa aga gca gag aag 1588

Gln Glu Ala Ala Gln Ser Arg Arg Glu Glu Lys Lys Arg Ala Glu Lys

430 435 440

gag cga atc atg aat gag gaa gat cct gag aaa cag cgc agg ctg gag 1636

Glu Arg Ile Met Asn Glu Glu Asp Pro Glu Lys Gln Arg Arg Leu Glu

445

450

455

gag gct gca ttg agg cgt gag caa aag aag ttg gaa aag aag caa atg 1684

Glu Ala Ala Leu Arg Arg Glu Gln Lys Lys Leu Glu Lys Lys Gln Met

460

465

470

aaa atg aaa caa atc aaa gtg aaa gcc atg taaagccatc ccagagattt 1734

Lys Met Lys Gln Ile Lys Val Lys Ala Met

475

480

gagttctgat gccacctgta agctctgaat tcacaggaaa catgaaaaac gccagtccat 1794

ttctcaacct taaatttcag acagtcttgg gcaactgaga aatccttatt tcatcatcta 1854

ctctgttttg gggtttgggt ttacagaga ttgaagatac ctggaaaggg ctctgtttca 1914

agaatttttt ttccagata atcaaattat ttgattatt ttataaaagg aatgatctat 1974

gaaatctgtg taggttttaa atattttaaa aattataata caaatcatca gtgcttttag 2034

tacttcagtg tttaaagaaa taccatgaaa tttataggta gataaccaga ttgttgcttt 2094

ttgttttaaac caagcagttg aaatggctat aaagactgac tctaaaccaa gattctgcaa 2154

ataatgattg gaattgcaca ataaacattg cttgatgttt t 2195

<211> 483

<212> PRT

<213> Homo sapiens

<400> 72

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Val Ser Glu Ala Lys Phe Asp Asp Phe Glu Asp Glu Glu Asp Ile Val

20 25 30

Glu Tyr Asp Asp Asn Asp Phe Ala Glu Phe Glu Asp Val Met Glu Asp

35 40 45

Ser Val Thr Glu Ser Pro Gln Arg Val Ile Ile Thr Glu Asp Asp Glu

50 55 60

Asp Glu Thr Thr Val Glu Leu Glu Gly Gln Asp Glu Asn Gln Glu Gly

65 70 75 80

Asp Phe Glu Asp Ala Asp Thr Gln Glu Gly Asp Thr Glu Ser Glu Pro

85 90 95

Tyr Asp Asp Glu Glu Phe Glu Gly Tyr Glu Asp Lys Pro Asp Thr Ser

100 105 110

Ser Ser Lys Asn Lys Asp Pro Ile Thr Ile Val Asp Val Pro Ala His

115 120 125

Leu Gln Asn Ser Trp Glu Ser Tyr Tyr Leu Glu Ile Leu Met Val Thr
130 135 140

Gly Leu Leu Ala Tyr Ile Met Asn Tyr Ile Ile Gly Lys Asn Lys Asn
145 150 155 160

Ser Arg Leu Ala Gln Ala Trp Phe Asn Thr His Arg Glu Leu Leu Glu
165 170 175

Ser Asn Phe Thr Leu Val Gly Asp Asp Gly Thr Asn Lys Glu Ala Thr
180 185 190

Ser Thr Gly Lys Leu Asn Gln Glu Asn Glu His Ile Tyr Asn Leu Trp
195 200 205

Cys Ser Gly Arg Val Cys Cys Glu Gly Met Leu Ile Gln Leu Arg Phe
210 215 220

Leu Lys Arg Gln Asp Leu Leu Asn Val Leu Ala Arg Met Met Arg Pro
225 230 235 240

Val Ser Asp Gln Val Gln Ile Lys Val Thr Met Asn Asp Glu Asp Met
245 250 255

Asp Thr Tyr Val Phe Ala Val Gly Thr Arg Lys Ala Leu Val Arg Leu
260 265 270

Gln Lys Glu Met Gln Asp Leu Ser Glu Phe Cys Ser Asp Lys Pro Lys
275 280 285

Ser Gly Ala Lys Tyr Gly Leu Pro Asp Ser Leu Ala Ile Leu Ser Glu
290 295 300

Met Gly Glu Val Thr Asp Gly Met Met Asp Thr Lys Met Val His Phe
305 310 315 320

Leu Thr His Tyr Ala Asp Lys Ile Glu Ser Val His Phe Ser Asp Gln
325 330 335

Phe Ser Gly Pro Lys Ile Met Gln Glu Glu Gly Gln Pro Leu Lys Leu
340 345 350

Pro Asp Thr Lys Arg Thr Leu Leu Phe Thr Phe Asn Val Pro Gly Ser
355 360 365

Gly Asn Thr Tyr Pro Lys Asp Met Glu Ala Leu Leu Pro Leu Met Asn
370 375 380

Met Val Ile Tyr Ser Ile Asp Lys Ala Lys Lys Phe Arg Leu Asn Arg
385 390 395 400

Glu Gly Lys Gln Lys Ala Asp Lys Asn Arg Ala Arg Val Glu Glu Asn
405 410 415

Phe Leu Lys Leu Thr His Val Gln Arg Gln Glu Ala Ala Gln Ser Arg
420 425 430

Arg Glu Glu Lys Lys Arg Ala Glu Lys Glu Arg Ile Met Asn Glu Glu

435

440

445

Asp Pro Glu Lys Gln Arg Arg Leu Glu Glu Ala Ala Leu Arg Arg Glu

450

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460

Gln Lys Lys Leu Glu Lys Lys Gln Met Lys Met Lys Gln Ile Lys Val

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470

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Lys Ala Met

<210> 73

<211> 1290

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (258)..(824)

<400> 73

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ccgggaagga ggcgtggata tggagctggc tgctgccaag tccggggccc gcgccgctgc 180

ctagcgcgtc ctggggactc tgtggggacg cgccccgcgc cgcggctcgg ggacccgtag 240

agccccggcgcg tgcgcgc atg gcc ctg ctc tcg cgc ccc gcg ctc acc ctc 290

Met Ala Leu Leu Ser Arg Pro Ala Leu Thr Leu

1

5

10

ctg ctc ctc ctc atg gcc gct gtt gtc agg tgc cag gag cag gcc cag 338

Leu Leu Leu Leu Met Ala Ala Val Val Arg Cys Gln Glu Gln Ala Gln

15

20

25

acc acc gac tgg aga gcc acc ctg aag acc atc cgg aac ggc gtt cat 386

Thr Thr Asp Trp Arg Ala Thr Leu Lys Thr Ile Arg Asn Gly Val His

30

35

40

aag ata gac acg tac ctg aac gcc gcc ttg gac ctc cta gga ggc gag 434

Lys Ile Asp Thr Tyr Leu Asn Ala Ala Leu Asp Leu Leu Gly Gly Glu

45

50

55

gac ggt ctc tgc cag tat aaa tgc agt gac gga tct aag cct ttc cca 482

Asp Gly Leu Cys Gln Tyr Lys Cys Ser Asp Gly Ser Lys Pro Phe Pro

60

65

70

75

cgt tat ggt tat aaa ccc tcc cca ccg aat gga tgt ggc tct cca ctg 530

Arg Tyr Gly Tyr Lys Pro Ser Pro Pro Asn Gly Cys Gly Ser Pro Leu

80

85

90

ttt ggt gtt cat ctt aac att ggt atc cct tcc ctg aca aag tgt tgc 578

Phe Gly Val His Leu Asn Ile Gly Ile Pro Ser Leu Thr Lys Cys Cys

95

100

105

aac caa cac gac agg tgc tat gag acc tgt ggc aaa agc aag aat gac 626

Asn Gln His Asp Arg Cys Tyr Glu Thr Cys Gly Lys Ser Lys Asn Asp

110

115

120

tgt gat gaa gaa ttc cag tat tgc ctc tcc aag atc tgc cga gat gta 674

Cys Asp Glu Glu Phe Gln Tyr Cys Leu Ser Lys Ile Cys Arg Asp Val

125

130

135

cag aaa aca cta gga cta act cag cat gtt cag gca tgt gaa aca aca 722

Gln Lys Thr Leu Gly Leu Thr Gln His Val Gln Ala Cys Glu Thr Thr

140

145

150

155

gtg gag ctc ttg ttt gac agt gtt ata cat tta ggt tgt aaa cca tat 770

Val Glu Leu Leu Phe Asp Ser Val Ile His Leu Gly Cys Lys Pro Tyr

160

165

170

ctg gac agc caa cga gcc gca tgc agg tgt cat tat gaa gaa aaa act 818

Leu Asp Ser Gln Arg Ala Ala Cys Arg Cys His Tyr Glu Glu Lys Thr

175

180

185

gat ctt taaaggagat gccgacagct agtgacagat gaagatggaa gaacataacc 874

Asp Leu

tttgacaaat aactaatgtt tttaacaacat aaaactgtct tatttttgtg aaaggattat 934

tttgagacct taaaataatt tataatcttga tggtaaaacc tcaaagcaaa aaaagtgagg 994

gagatagtga ggggagggca cgcttgtctt ctcaggtatc ttccccagca ttgctccctt 1054

acttagtatg ccaaagtgtct tgaccaatat caaaaacaag tgcttgttta gcggagaatt 1114

ttgaaaagag gaatatataa ctcaattttc acaaccacat ttaccaaaaa aagagatcaa 1174

atataaaatt catcataatg tctgttcaac attatcttat ttggaaaatg gggaaattat 1234

cacttacaag tatttgttta ctatgaaatt ttaaatacac atttatgcct agaagg 1290

<210> 74

<211> 189

<212> PRT

<213> Homo sapiens

<400> 74

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Ala Ala Val Val Arg Cys Gln Glu Gln Ala Gln Thr Thr Asp Trp Arg

20 25 30

Ala Thr Leu Lys Thr Ile Arg Asn Gly Val His Lys Ile Asp Thr Tyr

35 40 45

Leu Asn Ala Ala Leu Asp Leu Leu Gly Gly Glu Asp Gly Leu Cys Gln

50 55 60

Tyr Lys Cys Ser Asp Gly Ser Lys Pro Phe Pro Arg Tyr Gly Tyr Lys

65 70 75 80

Pro Ser Pro Pro Asn Gly Cys Gly Ser Pro Leu Phe Gly Val His Leu

85

90

95

Asn Ile Gly Ile Pro Ser Leu Thr Lys Cys Cys Asn Gln His Asp Arg

100

105

110

Cys Tyr Glu Thr Cys Gly Lys Ser Lys Asn Asp Cys Asp Glu Glu Phe

115

120

125

Gln Tyr Cys Leu Ser Lys Ile Cys Arg Asp Val Gln Lys Thr Leu Gly

130

135

140

Leu Thr Gln His Val Gln Ala Cys Glu Thr Thr Val Glu Leu Leu Phe

145

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Ala Ala Cys Arg Cys His Tyr Glu Glu Lys Thr Asp Leu

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185

<210> 75

<211> 3171

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (85)..(2304)

<400> 75

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Met Ala Glu Ser Arg Gly Arg Leu Tyr

1

5

ctt tgg atg tgc ttg gct gct gcg ctg gca tct ttc ctg atg gga ttt 159

Leu Trp Met Cys Leu Ala Ala Ala Leu Ala Ser Phe Leu Met Gly Phe

10

15

20

25

atg gtg ggc tgg ttt att aag cct ctc aaa gaa acg acc act tct gtg 207

Met Val Gly Trp Phe Ile Lys Pro Leu Lys Glu Thr Thr Thr Ser Val

30

35

40

cgc tat cat caa agt ata cgg tgg aaa ctg gta tcc gaa atg aaa gct 255

Arg Tyr His Gln Ser Ile Arg Trp Lys Leu Val Ser Glu Met Lys Ala

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gaa aac atc aaa tca ttt ctt cgt tct ttt aca aag ctt cct cat ctg 303

Glu Asn Ile Lys Ser Phe Leu Arg Ser Phe Thr Lys Leu Pro His Leu

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gca gga aca gaa caa aat ttc ttg ctt gcc aag aaa atc caa acc cag 351

Ala Gly Thr Glu Gln Asn Phe Leu Leu Ala Lys Lys Ile Gln Thr Gln

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80

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tgg aag aaa ttt gga cta gat tca gcc aag ttg gtt cat tat gat gtc 399

Trp Lys Lys Phe Gly Leu Asp Ser Ala Lys Leu Val His Tyr Asp Val

90 95 100 105

ctc tta tct tac ccc aat gag aca aat gcc aac tat ata tcg att gtg 447

Leu Leu Ser Tyr Pro Asn Glu Thr Asn Ala Asn Tyr Ile Ser Ile Val

110 115 120

gat gaa cat gaa act gag att ttc aaa aca tca tac ctt gaa cca cca 495

Asp Glu His Glu Thr Glu Ile Phe Lys Thr Ser Tyr Leu Glu Pro Pro

125 130 135

cca gat ggc tat gag aat gtt aca aat att gtg cca cca tat aat gct 543

Pro Asp Gly Tyr Glu Asn Val Thr Asn Ile Val Pro Pro Tyr Asn Ala

140 145 150

ttc tca gcc caa ggc atg cca gag gga gat ctt gta tat gtg aac tat 591

Phe Ser Ala Gln Gly Met Pro Glu Gly Asp Leu Val Tyr Val Asn Tyr

155 160 165

gct cgc act gaa gac ttt ttc aaa cta gaa aga gag atg ggc atc aac 639

Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Glu Met Gly Ile Asn

170 175 180 185

tgt act ggg aag att gtt att gca aga tat gga aaa atc ttc aga gga 687

Cys Thr Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Ile Phe Arg Gly

190 195 200

aat aaa gtt aaa aat gcc atg tta gca gga gcc ata gga atc atc ttg 735

Asn Lys Val Lys Asn Ala Met Leu Ala Gly Ala Ile Gly Ile Ile Leu

205

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tac tca gat cca gct gac tac ttt gct cct gag gta cag cca tat ccc 783

Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Glu Val Gln Pro Tyr Pro

220

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aaa gga tgg aat ctt cct gga act gca gcc cag aga gga aat gtg tta 831

Lys Gly Trp Asn Leu Pro Gly Thr Ala Ala Gln Arg Gly Asn Val Leu

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aat ttg aat ggt gct ggt gac cca ctc act cca ggc tat cca gca aaa 879

Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr Pro Ala Lys

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gaa tac act ttc aga ctt gat gtt gaa gaa gga gtg gga atc ccc cga 927

Glu Tyr Thr Phe Arg Leu Asp Val Glu Glu Gly Val Gly Ile Pro Arg

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ata cct gta cat ccc att gga tat aat gat gca gaa ata tta tta cgc 975

Ile Pro Val His Pro Ile Gly Tyr Asn Asp Ala Glu Ile Leu Leu Arg

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Tyr Leu Gly Gly Ile Ala Pro Pro Asp Lys Ser Trp Lys Gly Ala Leu

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aat gtg agt tat agt atc gga cct ggc ttt aca ggg agt gat tct ttc 1071

Asn Val Ser Tyr Ser Ile Gly Pro Gly Phe Thr Gly Ser Asp Ser Phe
315 320 325

agg aag gtt aga atg cat gtt tat aac atc aat aaa att aca agg att 1119
Arg Lys Val Arg Met His Val Tyr Asn Ile Asn Lys Ile Thr Arg Ile
330 335 340 345

tac aat gta gtt gga act atc aga gga tct gtg gaa cct gac agg tat 1167
Tyr Asn Val Val Gly Thr Ile Arg Gly Ser Val Glu Pro Asp Arg Tyr
350 355 360

gtt att ctg gga ggt cac cgg gac tcc tgg gta ttt gga gct att gac 1215
Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly Ala Ile Asp
365 370 375

cca acc agt ggg gtt gct gtt ttg caa gaa att gcc cgg agt ttt gga 1263
Pro Thr Ser Gly Val Ala Val Leu Gln Glu Ile Ala Arg Ser Phe Gly
380 385 390

aaa ctg atg agt aaa ggc tgg aga cct aga aga act atc att ttt gcc 1311
Lys Leu Met Ser Lys Gly Trp Arg Pro Arg Arg Thr Ile Ile Phe Ala
395 400 405

agc tgg gat gca gaa gaa ttt gga ctt ctg ggt tcc aca gaa tgg gct 1359
Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr Glu Trp Ala
410 415 420 425

gag gag aat gtc aaa ata ctc cag gag aga agc att gct tat atc aac 1407
Glu Glu Asn Val Lys Ile Leu Gln Glu Arg Ser Ile Ala Tyr Ile Asn

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tcg gat tca tct ata gaa ggc aat tat act ctc aga gtt gac tgt act 1455

Ser Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val Asp Cys Thr

445

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ccc ctt ctt tac caa tta gtg tat aaa ctg aca aaa gag atc ccc agc 1503

Pro Leu Leu Tyr Gln Leu Val Tyr Lys Leu Thr Lys Glu Ile Pro Ser

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cct gat gat ggg ttt gag agt aaa tca ctg tat gaa agc tgg ttg gaa 1551

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aaa gac cct tca cct gaa aat aaa aat ttg cct aga atc aat aag ctg 1599

Lys Asp Pro Ser Pro Glu Asn Lys Asn Leu Pro Arg Ile Asn Lys Leu

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495

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gga tct gga agt gac ttt gaa gct tat ttt cag aga ctt gga att gct 1647

Gly Ser Gly Ser Asp Phe Glu Ala Tyr Phe Gln Arg Leu Gly Ile Ala

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tca ggc aga gcc cgt tac act aag aat aag aaa aca gat aag tac agc 1695

Ser Gly Arg Ala Arg Tyr Thr Lys Asn Lys Lys Thr Asp Lys Tyr Ser

525

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agc tac cca gtg tac cac aca att tat gag aca ttt gaa ttg gta gag 1743

Ser Tyr Pro Val Tyr His Thr Ile Tyr Glu Thr Phe Glu Leu Val Glu

540

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aaa ttt tat gac ccc aca ttt aaa aaa caa ctt tct gtg gct caa tta 1791

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cga gga gca ctg gta tat gag ctt gtg gat tct aaa atc att cct ttt 1839

Arg Gly Ala Leu Val Tyr Glu Leu Val Asp Ser Lys Ile Ile Pro Phe

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575

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Asn Ile Gln Asp Tyr Ala Glu Ala Leu Lys Asn Tyr Ala Ala Ser Ile

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600

tat aat cta tct aag aaa cat gat caa caa ttg aca gac cat gga gta 1935

Tyr Asn Leu Ser Lys Lys His Asp Gln Gln Leu Thr Asp His Gly Val

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Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Ser Glu Ala Ala

620

625

630

tca gat ttt cat aaa cga ctt ata caa gtt gat ctt aac aat ccc att 2031

Ser Asp Phe His Lys Arg Leu Ile Gln Val Asp Leu Asn Asn Pro Ile

635

640

645

gca gtg aga atg atg aat gac caa ctg atg ctc ctg gaa aga gca ttc 2079

Ala Val Arg Met Met Asn Asp Gln Leu Met Leu Leu Glu Arg Ala Phe

650

655

660

665

atc gat cct ctt ggt tta cca gga aag ctg ttc tat agg cac atc ata 2127
Ile Asp Pro Leu Gly Leu Pro Gly Lys Leu Phe Tyr Arg His Ile Ile

670 675 680

ttt gct cca agt agc cac aac aaa tat gct gga gaa tca ttt cct gga 2175
Phe Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser Phe Pro Gly

685 690 695

atc tat gat gct atc ttt gat att gaa aat aaa gcc aac tct cgt ttg 2223
Ile Tyr Asp Ala Ile Phe Asp Ile Glu Asn Lys Ala Asn Ser Arg Leu

700 705 710

gcc tgg aaa gaa gta aag aaa cat att tct att gca gct ttt aca att 2271
Ala Trp Lys Glu Val Lys Lys His Ile Ser Ile Ala Ala Phe Thr Ile

715 720 725

caa gca gca gca gga act ctg aaa gaa gta tta tagaaggctt caagtggcta 2324
Gln Ala Ala Ala Gly Thr Leu Lys Glu Val Leu

730 735 740

gccattaaag gtgttgctaa aagctgagg ataaaattca ctttctgat aacttatgaa 2384

gccagggtgt tctaaactct ttcatgtca tgttttgatt ataggctttg gtcttttcat 2444

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<212> PRT

<213> Homo sapiens

<400> 76

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20 25 30

Pro Leu Lys Glu Thr Thr Thr Ser Val Arg Tyr His Gln Ser Ile Arg

35 40 45

Trp Lys Leu Val Ser Glu Met Lys Ala Glu Asn Ile Lys Ser Phe Leu

50 55 60

Arg Ser Phe Thr Lys Leu Pro His Leu Ala Gly Thr Glu Gln Asn Phe

65 70 75 80

Leu Leu Ala Lys Lys Ile Gln Thr Gln Trp Lys Lys Phe Gly Leu Asp

85 90 95

Ser Ala Lys Leu Val His Tyr Asp Val Leu Leu Ser Tyr Pro Asn Glu

100 105 110

Thr Asn Ala Asn Tyr Ile Ser Ile Val Asp Glu His Glu Thr Glu Ile

115 120 125

Phe Lys Thr Ser Tyr Leu Glu Pro Pro Pro Asp Gly Tyr Glu Asn Val

130 135 140

Thr Asn Ile Val Pro Pro Tyr Asn Ala Phe Ser Ala Gln Gly Met Pro

145 150 155 160

Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe
165 170 175

Lys Leu Glu Arg Glu Met Gly Ile Asn Cys Thr Gly Lys Ile Val Ile
180 185 190

Ala Arg Tyr Gly Lys Ile Phe Arg Gly Asn Lys Val Lys Asn Ala Met
195 200 205

Leu Ala Gly Ala Ile Gly Ile Ile Leu Tyr Ser Asp Pro Ala Asp Tyr
210 215 220

Phe Ala Pro Glu Val Gln Pro Tyr Pro Lys Gly Trp Asn Leu Pro Gly
225 230 235 240

Thr Ala Ala Gln Arg Gly Asn Val Leu Asn Leu Asn Gly Ala Gly Asp
245 250 255

Pro Leu Thr Pro Gly Tyr Pro Ala Lys Glu Tyr Thr Phe Arg Leu Asp
260 265 270

Val Glu Glu Gly Val Gly Ile Pro Arg Ile Pro Val His Pro Ile Gly
275 280 285

Tyr Asn Asp Ala Glu Ile Leu Leu Arg Tyr Leu Gly Gly Ile Ala Pro
290 295 300

Pro Asp Lys Ser Trp Lys Gly Ala Leu Asn Val Ser Tyr Ser Ile Gly
305 310 315 320

Pro Gly Phe Thr Gly Ser Asp Ser Phe Arg Lys Val Arg Met His Val

325

330

335

Tyr Asn Ile Asn Lys Ile Thr Arg Ile Tyr Asn Val Val Gly Thr Ile

340

345

350

Arg Gly Ser Val Glu Pro Asp Arg Tyr Val Ile Leu Gly Gly His Arg

355

360

365

Asp Ser Trp Val Phe Gly Ala Ile Asp Pro Thr Ser Gly Val Ala Val

370

375

380

Leu Gln Glu Ile Ala Arg Ser Phe Gly Lys Leu Met Ser Lys Gly Trp

385

390

395

400

Arg Pro Arg Arg Thr Ile Ile Phe Ala Ser Trp Asp Ala Glu Glu Phe

405

410

415

Gly Leu Leu Gly Ser Thr Glu Trp Ala Glu Glu Asn Val Lys Ile Leu

420

425

430

Gln Glu Arg Ser Ile Ala Tyr Ile Asn Ser Asp Ser Ser Ile Glu Gly

435

440

445

Asn Tyr Thr Leu Arg Val Asp Cys Thr Pro Leu Leu Tyr Gln Leu Val

450

455

460

Tyr Lys Leu Thr Lys Glu Ile Pro Ser Pro Asp Asp Gly Phe Glu Ser

465 470 475 480

Lys Ser Leu Tyr Glu Ser Trp Leu Glu Lys Asp Pro Ser Pro Glu Asn

485 490 495

Lys Asn Leu Pro Arg Ile Asn Lys Leu Gly Ser Gly Ser Asp Phe Glu

500 505 510

Ala Tyr Phe Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr

515 520 525

Lys Asn Lys Lys Thr Asp Lys Tyr Ser Ser Tyr Pro Val Tyr His Thr

530 535 540

Ile Tyr Glu Thr Phe Glu Leu Val Glu Lys Phe Tyr Asp Pro Thr Phe

545 550 555 560

Lys Lys Gln Leu Ser Val Ala Gln Leu Arg Gly Ala Leu Val Tyr Glu

565 570 575

Leu Val Asp Ser Lys Ile Ile Pro Phe Asn Ile Gln Asp Tyr Ala Glu

580 585 590

Ala Leu Lys Asn Tyr Ala Ala Ser Ile Tyr Asn Leu Ser Lys Lys His

595 600 605

Asp Gln Gln Leu Thr Asp His Gly Val Ser Phe Asp Ser Leu Phe Ser

610 615 620

Ala Val Lys Asn Phe Ser Glu Ala Ala Ser Asp Phe His Lys Arg Leu
625 630 635 640

Ile Gln Val Asp Leu Asn Asn Pro Ile Ala Val Arg Met Met Asn Asp
645 650 655

Gln Leu Met Leu Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro
660 665 670

Gly Lys Leu Phe Tyr Arg His Ile Ile Phe Ala Pro Ser Ser His Asn
675 680 685

Lys Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Ile Phe Asp
690 695 700

Ile Glu Asn Lys Ala Asn Ser Arg Leu Ala Trp Lys Glu Val Lys Lys
705 710 715 720

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Lys Glu Val Leu
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<400> 77

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gcgaggagcc atg agg cgc cag cct gcg aag gtg gcg gcg ctg ctg ctc 169

Met Arg Arg Gln Pro Ala Lys Val Ala Ala Leu Leu Leu

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ggg ctg ctc ttg gag tgc aca gaa gcc aaa aag cat tgc tgg tat ttc 217

Gly Leu Leu Leu Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe

15 20 25

gaa gga ctc tat cca acc tat tat ata tgc cgc tcc tac gag gac tgc 265

Glu Gly Leu Tyr Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys

30 35 40 45

tgt ggc tcc agg tgc tgt gtg cgg gcc ctc tcc ata cag agg ctg tgg 313

Cys Gly Ser Arg Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp

50 55 60

tac ttc tgg ttc ctt ctg atg atg ggc gtg ctt ttc tgc tgc gga gcc 361

Tyr Phe Trp Phe Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala

65 70 75

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Gly Phe Phe Ile Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu

80

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Pro Ala Phe Asn Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro

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gga acc cag cag ccg ggg ccg ccc tat tac acc gac cca gga gga ccg 505

Gly Thr Gln Gln Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro

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ggg atg aac cct gtc ggg aat tcc atg gca atg gct ttc cag gtc cca 553

Gly Met Asn Pro Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro

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ccc aac tca ccc cag ggg agt gtg gcc tgc ccg ccc cct cca gcc tac 601

Pro Asn Ser Pro Gln Gly Ser Val Ala Cys Pro Pro Pro Pro Ala Tyr

145

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Cys Asn Thr Pro Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys

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tgcaaaataa aaataaattt gggc 2890

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<212> PRT

<213> Homo sapiens

<400> 78

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Leu Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe Glu Gly Leu

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30

Tyr Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser

35

40

45

Arg Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp

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55

60

Phe Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe

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70

75

80

Ile Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe

85

90

95

Asn Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Thr Gln

100

105

110

Gln Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn

115

120

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Pro Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser

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Pro Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys

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<210> 79

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cctgacgcct gacgcctgta cccggccccg c atg agc cgc tac ctg ctg ccg 172

Met Ser Arg Tyr Leu Leu Pro

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ctg tcg gcg ctg ggc acg gta gca ggc gcc gcc gtg ctg ctc aag gac 220

Leu Ser Ala Leu Gly Thr Val Ala Gly Ala Ala Val Leu Leu Lys Asp

10

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tat gtc acc ggt ggg gct tgc ccc agc aag gcc acc atc cct ggg aag 268

Tyr Val Thr Gly Gly Ala Cys Pro Ser Lys Ala Thr Ile Pro Gly Lys

25

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35

acg gtc atc gtg acg ggc gcc aac aca ggc atc ggg aag cag acc gcc 316

Thr Val Ile Val Thr Gly Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala

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45

50

55

ttg gaa ctg gcc agg aga gga ggc aac atc atc ctg gcc tgc cga gac 364

Leu Glu Leu Ala Arg Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp

60	65	70	
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Met Glu Lys Cys Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu			
75	80	85	
aat cac cat gtc aac gcc cgg cac ctg gac ttg gct tcc ctc aag tct			460
Asn His His Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser			
90	95	100	
atc cga gtg ttt gca gca aag atc att gaa gag gag gag cga gtg gac			508
Ile Arg Val Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp			
105	110	115	
att cta atc aac aac gcg ggt gtg atg cgg tgc ccc cac tgg acc acc			556
Ile Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr			
120	125	130	135
gag gac ggc ttc gag atg cag ttt ggc gtt aac cac ctg ggt cac ttt			604
Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His Phe			
140	145	150	
ctc ttg aca aac ttg ctg ctg gac aag ctg aaa gcc tca gcc cct tcg			652
Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala Pro Ser			
155	160	165	
cgg atc atc aac ctc tcg tcc ctg gcc cat gtt gct ggg cac ata gac			700
Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly His Ile Asp			
170	175	180	

ttt gac gac ttg aac tgg cag acg agg aag tat aac acc aaa gcc gcc 748

Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn Thr Lys Ala Ala

185

190

195

tac tgc cag agc aag ctc gcc atc gtc ctc ttc acc aag gag ctg agc 796

Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe Thr Lys Glu Leu Ser

200

205

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215

cgg cgg ctg caa ggc tct ggt gtg act gtc aac gcc ctg cac ccc ggc 844

Arg Arg Leu Gln Gly Ser Gly Val Thr Val Asn Ala Leu His Pro Gly

220

225

230

gtg gcc agg aca gag ctg ggc aga cac acg ggc atc cat ggc tcc acc 892

Val Ala Arg Thr Glu Leu Gly Arg His Thr Gly Ile His Gly Ser Thr

235

240

245

ttc tcc agc acc aca ctc ggg ccc atc ttc tgg ctg ctg gtc aag agc 940

Phe Ser Ser Thr Thr Leu Gly Pro Ile Phe Trp Leu Leu Val Lys Ser

250

255

260

ccc gag ctg gcc gcc cag ccc agc aca tac ctg gcc gtg gcg gag gaa 988

Pro Glu Leu Ala Ala Gln Pro Ser Thr Tyr Leu Ala Val Ala Glu Glu

265

270

275

ctg gcg gat gtt tcc gga aag tac ttc gat gga ctc aaa cag aag gcc 1036

Leu Ala Asp Val Ser Gly Lys Tyr Phe Asp Gly Leu Lys Gln Lys Ala

280

285

290

295

ccg gcc ccc gag gct gag gat gag gag gtg gcc cgg agg ctt tgg gct 1084

Pro Ala Pro Glu Ala Glu Asp Glu Glu Val Ala Arg Arg Leu Trp Ala

300

305

310

gaa agt gcc cgc ctg gtg ggc tta gag gct ccc tct gtg agg gag cag 1132

Glu Ser Ala Arg Leu Val Gly Leu Glu Ala Pro Ser Val Arg Glu Gln

315

320

325

ccc ctc ccc aga taacctctgg agcagatttg aaagccagga tggcgcctcc 1184

Pro Leu Pro Arg

330

agaccgagga cagctgtccg ccatgcccgc agcttcctgg cactacctga gccgggagac 1244

ccaggactgg cggccgccat gccgcagta ggttctaggg ggcggtgctg gccgcagtgg 1304

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atgctcagaa taactgctgt ctcccatgat ggtgtggtac agcgagctgt tgtctggcta 1664

tggcatggct gtgccggggg tgtttgctga gggcttcctg tgccagagcc cagccagaga 1724

gcaggtgcag gtgtcatcct gatttcaggc tctgcacggc atggagtggg aaccccacca 1784

gctgctgcta caggacctgg gattgcctgg gactcccacc ttccatcaa ttctcatggt 1844

agtccaaact gcagactctc aaacttgctc attt 1878

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<211> 331

<212> PRT

<213> Homo sapiens

<400> 80

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1 5 10 15

Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys Pro Ser

20 25 30

Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly Ala Asn Thr

35 40 45

Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg Arg Gly Gly Asn

50 55 60

Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys Glu Ala Ala Ala Lys

65 70 75 80

Asp Ile Arg Gly Glu Thr Leu Asn His His Val Asn Ala Arg His Leu

85

90

95

Asp Leu Ala Ser Leu Lys Ser Ile Arg Val Phe Ala Ala Lys Ile Ile

100

105

110

Glu Glu Glu Glu Arg Val Asp Ile Leu Ile Asn Asn Ala Gly Val Met

115

120

125

Arg Cys Pro His Trp Thr Thr Glu Asp Gly Phe Glu Met Gln Phe Gly

130

135

140

Val Asn His Leu Gly His Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys

145

150

155

160

Leu Lys Ala Ser Ala Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala

165

170

175

His Val Ala Gly His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg

180

185

190

Lys Tyr Asn Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val

195

200

205

Leu Phe Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr

210

215

220

Val Asn Ala Leu His Pro Gly Val Ala Arg Thr Glu Leu Gly Arg His

225

230

235

240

Thr Gly Ile His Gly Ser Thr Phe Ser Ser Thr Thr Leu Gly Pro Ile
245 250 255

Phe Trp Leu Leu Val Lys Ser Pro Glu Leu Ala Ala Gln Pro Ser Thr
260 265 270

Tyr Leu Ala Val Ala Glu Glu Leu Ala Asp Val Ser Gly Lys Tyr Phe
275 280 285

Asp Gly Leu Lys Gln Lys Ala Pro Ala Pro Glu Ala Glu Asp Glu Glu
290 295 300

Val Ala Arg Arg Leu Trp Ala Glu Ser Ala Arg Leu Val Gly Leu Glu
305 310 315 320

Ala Pro Ser Val Arg Glu Gln Pro Leu Pro Arg
325 330

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<211> 2392

<212> DNA

<213> Homo sapiens

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<400> 81

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Met Ala Pro Ser Gly Ser Leu

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gca gtt ccc ctg gca gtc ctg gtg ctg ttg ctt tgg ggt gct ccc tgg 101

Ala Val Pro Leu Ala Val Leu Val Leu Leu Trp Gly Ala Pro Trp

10

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acg cac ggg cgg cgg agc aac gtt cgc gtc atc acg gac gag aac tgg 149

Thr His Gly Arg Arg Ser Asn Val Arg Val Ile Thr Asp Glu Asn Trp

25

30

35

aga gaa ctg ctg gaa gga gac tgg atg ata gaa ttt tat gcc ccg tgg 197

Arg Glu Leu Leu Glu Gly Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp

40

45

50

55

tgc cct gct tgt caa aat ctt caa ccg gaa tgg gaa agt ttt gct gaa 245

Cys Pro Ala Cys Gln Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu

60

65

70

tgg gga gaa gat ctt gag gtt aat att gcg aaa gta gat gtc aca gag 293

Trp Gly Glu Asp Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu

75

80

85

cag cca gga ctg agt gga cgg ttt atc ata act gct ctt cct act att 341

Gln Pro Gly Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile

90

95

100

tat cat tgt aaa gat ggt gaa ttt agg cgc tat cag ggt cca agg act 389

Tyr His Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr

105

110

115

aag aag gac ttc ata aac ttt ata agt gat aaa gag tgg aag agt att 437

Lys Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile

120

125

130

135

gag ccc gtt tca tca tgg ttt ggt cca ggt tct gtt ctg atg agt agt 485

Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser Ser

140

145

150

atg tca gca ctc ttt cag cta tct atg tgg atc agg acg tgc cat aac 533

Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys His Asn

155

160

165

tac ttt att gaa gac ctt gga ttg cca gcg tgg gga tca tat act gtt 581

Tyr Phe Ile Glu Asp Leu Gly Leu Pro Ala Trp Gly Ser Tyr Thr Val

170

175

180

ttt gct tta gca act ctg ttt tcc gga ctg tta tta gga ctc tgt atg 629

Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu Gly Leu Cys Met

185

190

195

ata ttt gtg gca gat tgc ctt tgt cct tca aaa agg cgc aga cca cag 677

Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys Arg Arg Arg Pro Gln

200

205

210

215

cca tac cca tac cct tca aaa aaa tta tta tca gaa tct gca caa cct 725

Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu Ser Glu Ser Ala Gln Pro

220

225

230

ttg aaa aaa gtg gag gag gaa caa gag gcg gat gaa gaa gat gtt tca 773

Leu Lys Lys Val Glu Glu Glu Gln Glu Ala Asp Glu Glu Asp Val Ser

235

240

245

gaa gaa gaa gct gaa agt aaa gaa gga aca aac aaa gac ttt cca cag 821

Glu Glu Glu Ala Glu Ser Lys Glu Gly Thr Asn Lys Asp Phe Pro Gln

250

255

260

aat gcc ata aga caa cgc tct ctg ggt cca tca ttg gcc aca gat aaa 869

Asn Ala Ile Arg Gln Arg Ser Leu Gly Pro Ser Leu Ala Thr Asp Lys

265

270

275

tcc tagttaaatt ttatagttat cttaatatta tgattttgat aaaaacagaa 922

Ser

280

gattgatcat tttgtttggt ttgaagtga ctgtgacttt tttgaatatt gcagggttca 982

gtctagattg tcattaaatt gaagagtcta cattcagaac ataaaagcac taggtataca 1042

agtttggaat atgatttaag cacagtatga tggtttaaat agttctctaa tttttgaaaa 1102

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aaatttcata ttatcctgtg ttctttcctg actggtaata ttgtgtggga tttcacaggt 2062

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agatttacag tatcgtaata tacaagtttt ctttaaagcc ctctccttta gaatttaaaa 2302

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cacaaaataa acctttctaa ccacttcatt 2392

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<211> 280

<212> PRT

<213> Homo sapiens

<400> 82

Met Ala Pro Ser Gly Ser Leu Ala Val Pro Leu Ala Val Leu Val Leu

1

5

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15

Leu Leu Trp Gly Ala Pro Trp Thr His Gly Arg Arg Ser Asn Val Arg

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30

Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly Asp Trp Met

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40

45

Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln Asn Leu Gln Pro

50

55

60

Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp Leu Glu Val Asn Ile
65 70 75 80

Ala Lys Val Asp Val Thr Glu Gln Pro Gly Leu Ser Gly Arg Phe Ile
85 90 95

Ile Thr Ala Leu Pro Thr Ile Tyr His Cys Lys Asp Gly Glu Phe Arg
100 105 110

Arg Tyr Gln Gly Pro Arg Thr Lys Lys Asp Phe Ile Asn Phe Ile Ser
115 120 125

Asp Lys Glu Trp Lys Ser Ile Glu Pro Val Ser Ser Trp Phe Gly Pro
130 135 140

Gly Ser Val Leu Met Ser Ser Met Ser Ala Leu Phe Gln Leu Ser Met
145 150 155 160

Trp Ile Arg Thr Cys His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro
165 170 175

Ala Trp Gly Ser Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly
180 185 190

Leu Leu Leu Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro
195 200 205

Ser Lys Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu

210

215

220

Leu Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu

225

230

235

240

Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu Gly

245

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Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser Leu Gly

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Pro Ser Leu Ala Thr Asp Lys Ser

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<210> 83

<211> 1821

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<213> Homo sapiens

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ccggccaggg agggcc atg att tcc ctc ccg ggg ccc ctg gtg acc aac ttg 172

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu

1

5

10

ctg cgg ttt ttg ttc ctg ggg ctg agt gcc ctc gcg ccc ccc tcg cgg 220

Leu Arg Phe Leu Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg

15

20

25

gcc cag ctg caa ctg cac ttg ccc gcc aac cgg ttg cag gcg gtg gag 268

Ala Gln Leu Gln Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu

30

35

40

gga ggg gaa gtg gtg ctt cca gcg tgg tac acc ttg cac ggg gag gtg 316

Gly Gly Glu Val Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val

45

50

55

60

tct tca tcc cag cca tgg gag gtg ccc ttt gtg atg tgg ttc ttc aaa 364

Ser Ser Ser Gln Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys

65

70

75

cag aaa gaa aag gag gat cag gtg ttg tcc tac atc aat ggg gtc aca 412

Gln Lys Glu Lys Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr

80

85

90

aca agc aaa cct gga gta tcc ttg gtc tac tcc atg ccc tcc cgg aac 460

Thr Ser Lys Pro Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn

95

100

105

ctg tcc ctg cgg ctg gag ggt ctc cag gag aaa gac tct ggc ccc tac 508

Leu Ser Leu Arg Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr

110

115

120

agc tgc tcc gtg aat gtg caa gac aaa caa ggc aaa tct agg ggc cac 556

Ser Cys Ser Val Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His

125

130

135

140

agc atc aaa acc tta gaa ctc aat gta ctg gtt cct cca gct cct cca 604

Ser Ile Lys Thr Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro

145

150

155

tcc tgc cgt ctc cag ggt gtg ccc cat gtg ggg gca aac gtg acc ctg 652

Ser Cys Arg Leu Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu

160

165

170

agc tgc cag tct cca agg agt aag ccc gct gtc caa tac cag tgg gat 700

Ser Cys Gln Ser Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp

175

180

185

cgg cag ctt cca tcc ttc cag act ttc ttt gca cca gca tta gat gtc 748

Arg Gln Leu Pro Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val

190

195

200

atc cgt ggg tct tta agc ctc acc aac ctt tcg tct tcc atg gct gga 796

Ile Arg Gly Ser Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly

205

210

215

220

gtc tat gtc tgc aag gcc cac aat gag gtg ggc act gcc caa tgt aat 844

Val Tyr Val Cys Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn

225	230	235	
gtg acg ctg gaa gtg agc aca ggg cct gga gct gca gtg gtt gct gga			892
Val Thr Leu Glu Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly			
240	245	250	
gct gtt gtg ggt acc ctg gtt gga ctg ggg ttg ctg gct ggg ctg gtc			940
Ala Val Val Gly Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val			
255	260	265	
ctc ttg tac cac cgc cgg ggc aag gcc ctg gag gag cca gcc aat gat			988
Leu Leu Tyr His Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp			
270	275	280	
atc aag gag gat gcc att gct ccc cgg acc ctg ccc tgg ccc aag agc			1036
Ile Lys Glu Asp Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser			
285	290	295	300
tca gac aca atc tcc aag aat ggg acc ctt tcc tct gtc acc tcc gca			1084
Ser Asp Thr Ile Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala			
305	310	315	

cga gcc ctc cgg cca ccc cat ggc cct ccc agg cct ggt gca ttg acc			1132
Arg Ala Leu Arg Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr			
320	325	330	
ccc acg ccc agt ctc tcc agc cag gcc ctg ccc tca cca aga ctg ccc			1180
Pro Thr Pro Ser Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro			
335	340	345	

acg aca gat ggg gcc cac cct caa cca ata tcc ccc atc cct ggt ggg 1228

Thr Thr Asp Gly Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly

350

355

360

gtt tct tcc tct ggc ttg agc cgc atg ggt gct gtg cct gtg atg gtg 1276

Val Ser Ser Ser Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val

365

370

375

380

cct gcc cag agt caa gct ggc tct ctg gta tgatgacccc accactcatt 1326

Pro Ala Gln Ser Gln Ala Gly Ser Leu Val

385

390

ggctaaagga ttggggtct ctcccttccta taagggtcac ctctagcaca gaggcctgag 1386

tcatgggaaa gagtcacact cctgaccctt agtactctgc cccacctct ctttactgtg 1446

ggaaaaccat ctcaagtaaga cctaagtgtc caggagacag aaggagaaga ggaagtggat 1506

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taatgtttgt atgag

1821

<210> 84

<211> 390

<212> PRT

<213> Homo sapiens

<400> 84

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1 5 10 15

Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln

20 25 30

Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val

35 40 45

Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln

50 55 60

Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys

65 70 75 80

Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro

85 90 95

Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg

100 105 110

Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val

115

120

125

Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr

130

135

140

Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu

145

150

155

160

Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser

165

170

175

Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro

180

185

190

Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser

195

200

205

Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys

210

215

220

Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu

225

230

235

240

Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly

245

250

255

Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His

260

265

270

Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp

275

280

285

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile

290

295

300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg

305

310

315

320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser

325

330

335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly

340

345

350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser

355

360

365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser

370

375

380

Gln Ala Gly Ser Leu Val

385

390

<210> 85

<211> 1808

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (85)..(1407)

<400> 85

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ccagagcctg gcctgggagc cagg atg gcc atc cac aaa gcc ttg gtg atg 111

Met Ala Ile His Lys Ala Leu Val Met

1

5

tgc ctg gga ctg cct ctc ttc ctg ttc cca ggg gcc tgg gcc cag ggc 159

Cys Leu Gly Leu Pro Leu Phe Leu Phe Pro Gly Ala Trp Ala Gln Gly

10

15

20

25

cat gtc cca ccc ggc tgc agc caa ggc ctc aac ccc ctg tac tac aac 207

His Val Pro Pro Gly Cys Ser Gln Gly Leu Asn Pro Leu Tyr Tyr Asn

30

35

40

ctg tgt gac cgc tct ggg gcg tgg ggc atc gtc ctg gag gcc gtg gct 255

Leu Cys Asp Arg Ser Gly Ala Trp Gly Ile Val Leu Glu Ala Val Ala

45

50

55

ggg gcg ggc att gtc acc acg ttt gtg ctc acc atc atc ctg gtg gcc 303

Gly Ala Gly Ile Val Thr Thr Phe Val Leu Thr Ile Ile Leu Val Ala

60

65

70

agc ctc ccc ttt gtg cag gac acc aag aaa cgg agc ctg ctg ggg acc 351
Ser Leu Pro Phe Val Gln Asp Thr Lys Lys Arg Ser Leu Leu Gly Thr

75

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cag gta ttc ttc ctt ctg ggg acc ctg ggc ctc ttc tgc ctc gtg ttt 399
Gln Val Phe Phe Leu Leu Gly Thr Leu Gly Leu Phe Cys Leu Val Phe

90

95

100

105

gcc tgt gtg gtg aag ccc gac ttc tcc acc tgt gcc tct cgg cgc ttc 447
Ala Cys Val Val Lys Pro Asp Phe Ser Thr Cys Ala Ser Arg Arg Phe

110

115

120

ctc ttt ggg gtt ctg ttc gcc atc tgc ttc tct tgt ctg gcg gct cac 495
Leu Phe Gly Val Leu Phe Ala Ile Cys Phe Ser Cys Leu Ala Ala His

125

130

135

gtc ttt gcc ctc aac ttc ctg gcc cgg aag aac cac ggg ccc cgg ggc 543
Val Phe Ala Leu Asn Phe Leu Ala Arg Lys Asn His Gly Pro Arg Gly

140

145

150

tgg gtg atc ttc act gtg gct ctg ctg ctg acc ctg gta gag gtc atc 591
Trp Val Ile Phe Thr Val Ala Leu Leu Leu Thr Leu Val Glu Val Ile

155

160

165

atc aat aca gag tgg ctg atc atc acc ctg gtt cgg ggc agt ggc gag 639
Ile Asn Thr Glu Trp Leu Ile Ile Thr Leu Val Arg Gly Ser Gly Glu

170

175

180

185

ggc ggc cct cag ggc aac agc agc gca ggc tgg gcc gtg gcc tcc ccc 687

Gly Gly Pro Gln Gly Asn Ser Ser Ala Gly Trp Ala Val Ala Ser Pro

190

195

200

tgt gcc atc gcc aac atg gac ttt gtc atg gca ctc atc tac gtc atg 735

Cys Ala Ile Ala Asn Met Asp Phe Val Met Ala Leu Ile Tyr Val Met

205

210

215

ctg ctg ctg ctg ggt gcc ttc ctg ggg gcc tgg ccc gcc ctg tgt ggc 783

Leu Leu Leu Leu Gly Ala Phe Leu Gly Ala Trp Pro Ala Leu Cys Gly

220

225

230

cgc tac aag cgc tgg cgt aag cat ggg gtc ttt gtg ctc ctc acc aca 831

Arg Tyr Lys Arg Trp Arg Lys His Gly Val Phe Val Leu Leu Thr Thr

235

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gcc acc tcc gtt gcc ata tgg gtg gtg tgg atc gtc atg tat act tac 879

Ala Thr Ser Val Ala Ile Trp Val Val Trp Ile Val Met Tyr Thr Tyr

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ggc aac aag cag cac aac agt ccc acc tgg gat gac ccc acg ctg gcc 927

Gly Asn Lys Gln His Asn Ser Pro Thr Trp Asp Asp Pro Thr Leu Ala

270

275

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atc gcc ctc gcc gcc aat gcc tgg gcc ttc gtc ctc ttc tac gtc atc 975

Ile Ala Leu Ala Ala Asn Ala Trp Ala Phe Val Leu Phe Tyr Val Ile

285

290

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ccc gag gtc tcc cag gtg acc aag tcc agc cca gag caa agc tac cag 1023

Pro Glu Val Ser Gln Val Thr Lys Ser Ser Pro Glu Gln Ser Tyr Gln
300 305 310

ggg gac atg tac ccc acc cgg ggc gtg ggc tat gag acc atc ctg aaa 1071
Gly Asp Met Tyr Pro Thr Arg Gly Val Gly Tyr Glu Thr Ile Leu Lys
315 320 325

gag cag aag ggt cag agc atg ttc gtg gag aac aag gcc ttt tcc atg 1119
Glu Gln Lys Gly Gln Ser Met Phe Val Glu Asn Lys Ala Phe Ser Met
330 335 340 345

gat gag ccg gtt gca gct aag agg ccg gtg tca cca tac agc ggg tac 1167
Asp Glu Pro Val Ala Ala Lys Arg Pro Val Ser Pro Tyr Ser Gly Tyr
350 355 360

aat ggg cag ctg ctg acc agt gtg tac cag ccc act gag atg gcc ctg 1215
Asn Gly Gln Leu Leu Thr Ser Val Tyr Gln Pro Thr Glu Met Ala Leu
365 370 375

atg cac aaa gtt ccg tcc gaa gga gct tac gac atc atc ctc cca cgg 1263
Met His Lys Val Pro Ser Glu Gly Ala Tyr Asp Ile Ile Leu Pro Arg

380 385 390

gcc acc gcc aac agc cag gtg atg ggc agt gcc aac tcg acc ctg cgg 1311
Ala Thr Ala Asn Ser Gln Val Met Gly Ser Ala Asn Ser Thr Leu Arg
395 400 405

gct gaa gac atg tac tcg gcc cag agc cac cag gcg gcc aca ccg ccg 1359
Ala Glu Asp Met Tyr Ser Ala Gln Ser His Gln Ala Ala Thr Pro Pro

410

415

420

425

aaa gac ggc aag aac tct cag gtc ttt aga aac ccc tac gtg tgg gac 1407

Lys Asp Gly Lys Asn Ser Gln Val Phe Arg Asn Pro Tyr Val Trp Asp

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tgagtcagcg gtggcgagga gaggcggtcg gatttgggga gggccctgag gacctggccc 1467

gggcaaggga ctctccaggc tcctcctccc cctggcaggc ccagcaacat gtgccccaga 1527

tgtggaaggg cctccctctc tgccagtgtt tgggtgggtg tcatgggtgt cccacccac 1587

tcctcagtgt ttgtggagtc gaggagccaa cccagcctc ctgccaggat cacctcggcg 1647

gtcacactcc agccaaatag tgttctcggg gtgggtggctg ggcagcgcct atgtttctct 1707

ggagattcct gcaacctcaa gagacttccc aggcgctcag gcctggatct tgctcctctg 1767

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<212> PRT

<213> Homo sapiens

<400> 86

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Leu Phe Pro Gly Ala Trp Ala Gln Gly His Val Pro Pro Gly Cys Ser

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30

Gln Gly Leu Asn Pro Leu Tyr Tyr Asn Leu Cys Asp Arg Ser Gly Ala

35

40

45

Trp Gly Ile Val Leu Glu Ala Val Ala Gly Ala Gly Ile Val Thr Thr

50

55

60

Phe Val Leu Thr Ile Ile Leu Val Ala Ser Leu Pro Phe Val Gln Asp

65

70

75

80

Thr Lys Lys Arg Ser Leu Leu Gly Thr Gln Val Phe Phe Leu Leu Gly

85

90

95

Thr Leu Gly Leu Phe Cys Leu Val Phe Ala Cys Val Val Lys Pro Asp

100

105

110

Phe Ser Thr Cys Ala Ser Arg Arg Phe Leu Phe Gly Val Leu Phe Ala

115

120

125

Ile Cys Phe Ser Cys Leu Ala Ala His Val Phe Ala Leu Asn Phe Leu

130

135

140

Ala Arg Lys Asn His Gly Pro Arg Gly Trp Val Ile Phe Thr Val Ala

145

150

155

160

Leu Leu Leu Thr Leu Val Glu Val Ile Ile Asn Thr Glu Trp Leu Ile

165

170

175

Ile Thr Leu Val Arg Gly Ser Gly Glu Gly Gly Pro Gln Gly Asn Ser

180

185

190

Ser Ala Gly Trp Ala Val Ala Ser Pro Cys Ala Ile Ala Asn Met Asp

195

200

205

Phe Val Met Ala Leu Ile Tyr Val Met Leu Leu Leu Leu Gly Ala Phe

210

215

220

Leu Gly Ala Trp Pro Ala Leu Cys Gly Arg Tyr Lys Arg Trp Arg Lys

225

230

235

240

His Gly Val Phe Val Leu Leu Thr Thr Ala Thr Ser Val Ala Ile Trp

245

250

255

Val Val Trp Ile Val Met Tyr Thr Tyr Gly Asn Lys Gln His Asn Ser

260

265

270

Pro Thr Trp Asp Asp Pro Thr Leu Ala Ile Ala Leu Ala Ala Asn Ala

275

280

285

Trp Ala Phe Val Leu Phe Tyr Val Ile Pro Glu Val Ser Gln Val Thr

290

295

300

Lys Ser Ser Pro Glu Gln Ser Tyr Gln Gly Asp Met Tyr Pro Thr Arg

305

310

315

320

Gly Val Gly Tyr Glu Thr Ile Leu Lys Glu Gln Lys Gly Gln Ser Met
325 330 335

Phe Val Glu Asn Lys Ala Phe Ser Met Asp Glu Pro Val Ala Ala Lys
340 345 350

Arg Pro Val Ser Pro Tyr Ser Gly Tyr Asn Gly Gln Leu Leu Thr Ser
355 360 365

Val Tyr Gln Pro Thr Glu Met Ala Leu Met His Lys Val Pro Ser Glu
370 375 380

Gly Ala Tyr Asp Ile Ile Leu Pro Arg Ala Thr Ala Asn Ser Gln Val
385 390 395 400

Met Gly Ser Ala Asn Ser Thr Leu Arg Ala Glu Asp Met Tyr Ser Ala
405 410 415

Gln Ser His Gln Ala Ala Thr Pro Pro Lys Asp Gly Lys Asn Ser Gln
420 425 430

Val Phe Arg Asn Pro Tyr Val Trp Asp
435 440

<210> 87

<211> 2015

<212> DNA

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<400> 87

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Met Trp Arg Cys Pro

1 5

ctg ggg cta ctg ctg ttg ctg ccg ctg gct ggc cac ttg gct ctg ggt 162

Leu Gly Leu Leu Leu Leu Leu Pro Leu Ala Gly His Leu Ala Leu Gly

10 15 20

gcc cag cag ggt cgt ggg cgc cgg gag cta gca ccg ggt ctg cac ctg 210

Ala Gln Gln Gly Arg Gly Arg Arg Glu Leu Ala Pro Gly Leu His Leu

25 30 35

cgg ggc atc cgg gac gcg gga ggc cgg tac tgc cag gag cag gac ctg 258

Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys Gln Glu Gln Asp Leu

40 45 50

tgc tgc cgc ggc cgt gcc gac gac tgt gcc ctg ccc tac ctg ggc gcc 306

Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu Pro Tyr Leu Gly Ala

55 60 65

atc tgt tac tgt gac ctc ttc tgc aac cgc acg gtc tcc gac tgc tgc 354

Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr Val Ser Asp Cys Cys
70 75 80 85

cct gac ttc tgg gac ttc tgc ctc ggc gtg cca ccc cct ttt ccc ccg 402
Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro Pro Pro Phe Pro Pro
90 95 100

atc caa gga tgt atg cat gga ggt cgt atc tat cca gtc ttg gga acg 450
Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr Pro Val Leu Gly Thr
105 110 115

tac tgg gac aac tgt aac cgt tgc acc tgc cag gag aac agg cag tgg 498
Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln Glu Asn Arg Gln Trp
120 125 130

cag tgt gac caa gaa cca tgc ctg gtg gat cca gac atg atc aaa gcc 546
Gln Cys Asp Gln Glu Pro Cys Leu Val Asp Pro Asp Met Ile Lys Ala
135 140 145

atc aac cag ggc aac tat ggc tgg cag gct ggg aac cac agc gcc ttc 594

~~Ile Asn Gln Gly Asn Tyr Gly Trp Gln Ala Gly Asn His Ser Ala Phe~~

150 155 160 165

tgg ggc atg acc ctg gat gag ggc att cgc tac cgc ctg ggc acc atc 642
Trp Gly Met Thr Leu Asp Glu Gly Ile Arg Tyr Arg Leu Gly Thr Ile
170 175 180

cgc cca tct tcc tcg gtc atg aac atg cat gaa att tat aca gtg ctg 690
Arg Pro Ser Ser Ser Val Met Asn Met His Glu Ile Tyr Thr Val Leu

185

190

195

aac cca ggg gag gtg ctt ccc aca gcc ttc gag gcc tct gag aag tgg 738

Asn Pro Gly Glu Val Leu Pro Thr Ala Phe Glu Ala Ser Glu Lys Trp

200

205

210

ccc aac ctg att cat gag cct ctt gac caa ggc aac tgt gca ggc tcc 786

Pro Asn Leu Ile His Glu Pro Leu Asp Gln Gly Asn Cys Ala Gly Ser

215

220

225

tgg gcc ttc tcc aca gca gct gtg gca tcc gat cgt gtc tca atc cat 834

Trp Ala Phe Ser Thr Ala Ala Val Ala Ser Asp Arg Val Ser Ile His

230

235

240

245

tct ctg gga cac atg acg cct gtc ctg tcg ccc cag aac ctg ctg tct 882

Ser Leu Gly His Met Thr Pro Val Leu Ser Pro Gln Asn Leu Leu Ser

250

255

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tgt gac acc cac cag cag cag ggc tgc cgc ggt ggg cgt ctc gat ggt 930

Cys Asp Thr His Gln Gln Gln Gly Cys Arg Gly Gly Arg Leu Asp Gly

265

270

275

gcc tgg tgg ttc ctg cgt cgc cga ggg gtg gtg tct gac cac tgc tac 978

Ala Trp Trp Phe Leu Arg Arg Arg Gly Val Val Ser Asp His Cys Tyr

280

285

290

ccc ttc tcg ggc cgt gaa cga gac gag gct ggc cct gcg ccc ccc tgt 1026

Pro Phe Ser Gly Arg Glu Arg Asp Glu Ala Gly Pro Ala Pro Pro Cys

295

300

305

atg atg cac agc cga gcc atg ggt cgg ggc aag cgc cag gcc act gcc 1074

Met Met His Ser Arg Ala Met Gly Arg Gly Lys Arg Gln Ala Thr Ala

310 315 320 325

cac tgc ccc aac agc tat gtt aat aac aat gac atc tac cag gtc act 1122

His Cys Pro Asn Ser Tyr Val Asn Asn Asn Asp Ile Tyr Gln Val Thr

330 335 340

cct gtc tac cgc ctc ggc tcc aac gac aag gag atc atg aag gag ctg 1170

Pro Val Tyr Arg Leu Gly Ser Asn Asp Lys Glu Ile Met Lys Glu Leu

345 350 355

atg gag aat ggc cct gtc caa gcc ctc atg gag gtg cat gag gac ttc 1218

Met Glu Asn Gly Pro Val Gln Ala Leu Met Glu Val His Glu Asp Phe

360 365 370

ttc cta tac aag gga ggc atc tac agc cac acg cca gtg agc ctt ggg 1266

Phe Leu Tyr Lys Gly Gly Ile Tyr Ser His Thr Pro Val Ser Leu Gly

375 380 385

agg cca gag aga tac cgc cgg cat ggg acc cac tca gtc aag atc aca 1314

Arg Pro Glu Arg Tyr Arg Arg His Gly Thr His Ser Val Lys Ile Thr

390 395 400 405

gga tgg gga gag gag acg ctg cca gat gga agg acg ctc aaa tac tgg 1362

Gly Trp Gly Glu Glu Thr Leu Pro Asp Gly Arg Thr Leu Lys Tyr Trp

410 415 420

act gcg gcc aac tcc tgg ggc cca gcc tgg ggc gag agg ggc cac ttc 1410

Thr Ala Ala Asn Ser Trp Gly Pro Ala Trp Gly Glu Arg Gly His Phe

425

430

435

cgc atc gtg cgc ggc gtc aat gag tgc gac atc gag agc ttc gtg ctg 1458

Arg Ile Val Arg Gly Val Asn Glu Cys Asp Ile Glu Ser Phe Val Leu

440

445

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ggc gtc tgg ggc cgc gtg ggc atg gag gac atg ggt cat cac 1500

Gly Val Trp Gly Arg Val Gly Met Glu Asp Met Gly His His

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ggccccaatg gggcgggtgac ccagcctcg ccgacagag ccgggggcgc aggcggggcgc 1620

cagggcgcta atcccggcgc gggttccgct gacgcagcgc ccgcctggg agccgcgggc 1680

aggcgagact ggcggagccc ccagacctcc cagtggggac ggggcagggc ctggcctggg 1740

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ccacacctgg ctaatTTTTTg tattttttgt aaagaggggg gtctcactgt gttgcccagg 1860

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2015

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<211> 467

<212> PRT

<213> Homo sapiens

<400> 88

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His Leu Ala Leu Gly Ala Gln Gln Gly Arg Gly Arg Arg Glu Leu Ala

20 25 30

Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys

35 40 45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu

50 55 60

~~Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr~~

65 70 75 80

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro

85 90 95

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr

100 105 110

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln

115

120

125

Glu Asn Arg Gln Trp Gln Cys Asp Gln Glu Pro Cys Leu Val Asp Pro

130

135

140

Asp Met Ile Lys Ala Ile Asn Gln Gly Asn Tyr Gly Trp Gln Ala Gly

145

150

155

160

Asn His Ser Ala Phe Trp Gly Met Thr Leu Asp Glu Gly Ile Arg Tyr

165

170

175

Arg Leu Gly Thr Ile Arg Pro Ser Ser Ser Val Met Asn Met His Glu

180

185

190

Ile Tyr Thr Val Leu Asn Pro Gly Glu Val Leu Pro Thr Ala Phe Glu

195

200

205

Ala Ser Glu Lys Trp Pro Asn Leu Ile His Glu Pro Leu Asp Gln Gly

210

215

220

Asn Cys Ala Gly Ser Trp Ala Phe Ser Thr Ala Ala Val Ala Ser Asp

225

230

235

240

Arg Val Ser Ile His Ser Leu Gly His Met Thr Pro Val Leu Ser Pro

245

250

255

Gln Asn Leu Leu Ser Cys Asp Thr His Gln Gln Gln Gly Cys Arg Gly

260

265

270

Gly Arg Leu Asp Gly Ala Trp Trp Phe Leu Arg Arg Arg Gly Val Val
275 280 285

Ser Asp His Cys Tyr Pro Phe Ser Gly Arg Glu Arg Asp Glu Ala Gly
290 295 300

Pro Ala Pro Pro Cys Met Met His Ser Arg Ala Met Gly Arg Gly Lys
305 310 315 320

Arg Gln Ala Thr Ala His Cys Pro Asn Ser Tyr Val Asn Asn Asn Asp
325 330 335

Ile Tyr Gln Val Thr Pro Val Tyr Arg Leu Gly Ser Asn Asp Lys Glu
340 345 350

Ile Met Lys Glu Leu Met Glu Asn Gly Pro Val Gln Ala Leu Met Glu
355 360 365

Val His Glu Asp Phe Phe Leu Tyr Lys Gly Gly Ile Tyr Ser His Thr
370 375 380

Pro Val Ser Leu Gly Arg Pro Glu Arg Tyr Arg Arg His Gly Thr His
385 390 395 400

Ser Val Lys Ile Thr Gly Trp Gly Glu Glu Thr Leu Pro Asp Gly Arg
405 410 415

Thr Leu Lys Tyr Trp Thr Ala Ala Asn Ser Trp Gly Pro Ala Trp Gly

420

425

430

Glu Arg Gly His Phe Arg Ile Val Arg Gly Val Asn Glu Cys Asp Ile

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Glu Ser Phe Val Leu Gly Val Trp Gly Arg Val Gly Met Glu Asp Met

450

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Gly His His

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<210> 89

<211> 1722

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (64)..(1692)

<400> 89

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aag atg ctg ctg cgc tcg aag cct gcg ctg ccg ccg ctg atg ctg 108

Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu

1

5

10

15

ctg ctc ctg ggg ccg ctg ggt ccc ctc tcc cct ggc gcc ctg ccc cga 156

Leu Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg

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cct gcg caa gca cag gac gtc gtg gac ctg gac ttc ttc acc cag gag 204

Pro Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu

35

40

45

ccg ctg cac ctg gtg agc ccc tcg ttc ctg tcc gtc acc att gac gcc 252

Pro Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala

50

55

60

aac ctg gcc acg gac ccg cgg ttc ctc atc ctc ctg ggt tct cca aag 300

Asn Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys

65

70

75

ctt cgt acc ttg gcc aga ggc ttg tct cct gcg tac ctg agg ttt ggt 348

Leu Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly

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ggc acc aag aca gac ttc cta att ttc gat ccc aag aag gaa tca acc 396

Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr

100

105

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ttt gaa gag aga agt tac tgg caa tct caa gtc aac cag gat att tgc 444

Phe Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys

115

120

125

aaa tat gga tcc atc cct cct gat gtg gag gag aag tta cgg ttg gaa 492

Lys Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu

130

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tgg ccc tac cag gag caa ttg cta ctc cga gaa cac tac cag aaa aag 540

Trp Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys

145

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ttc aag aac agc acc tac tca aga agc tct gta gat gtg cta tac act 588

Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr

160

165

170

175

ttt gca aac tgc tca gga ctg gac ttg atc ttt ggc cta aat gcg tta 636

Phe Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu

180

185

190

tta gga aca gca gat ttg cag tgg aac agt tct aat gct cag ttg ctc 684

Leu Gly Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu

195

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205

ctg gac tac tgc tct tcc aag ggg tat aac att tct tgg gaa cta ggc 732

Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly

210

215

220

aat gaa cct aac agt ttc ctt aag aag gct gat att ttc atc aat ggc 780

Asn Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly

225

230

235

tcg cag tta gga gaa gat ttt att caa ttg cat aaa ctt cta aga aag 828

Ser Gln Leu Gly Glu Asp Phe Ile Gln Leu His Lys Leu Leu Arg Lys

240

245

250

255

tcc acc ttc aaa aat gca aaa ctc tat ggt cct gat gtt ggt cag cct 876

Ser Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro

260

265

270

cga aga aag acg gct aag atg ctg aag agc ttc ctg aag gct ggt gga 924

Arg Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly

275

280

285

gaa gtg att gat tca gtt aca tgg cat cac tac tat ttg aat gga cgg 972

Glu Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg

290

295

300

act gct acc agg gaa gat ttt cta aac cct gat gta ttg gac att ttt 1020

Thr Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe

305

310

315

att tca tct gtg caa aaa gtt ttc cag gtg gtt gag agc acc agg cct 1068

Ile Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro

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325

330

335

ggc aag aag gtc tgg tta gga gaa aca agc tct gca cat gga ggc gga 1116

Gly-Lys Lys Val Trp Leu Gly-Glu Thr Ser Ser Ala His Gly Gly Gly

340

345

350

gcg ccc ttg cta tcc gac acc ttt gca gct ggc ttt atg tgg ctg gat 1164

Ala Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp

355

360

365

aaa ttg ggc ctg tca gcc cga atg gga ata gaa gtg gtg atg agg caa 1212

Lys Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln

370

375

380

gta ttc ttt gga gca gga aac tac cat tta gtg gat gaa aac ttc gat 1260

Val Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp

385

390

395

cct tta cct gat tat tgg cta tct ctt ctg ttc aag aaa ttg gtg ggc 1308

Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly

400

405

410

415

acc aag gtg tta atg gca agc gtg caa ggt tca aag aga agg aag ctt 1356

Thr Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu

420

425

430

cga gta tac ctt cat tgc aca aac act gac aat cca agg tat aaa gaa 1404

Arg Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu

435

440

445

~~gga gat tta act ctg tat gcc ata aac ctc cat aat gtc acc aag tac 1452~~

Gly Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr

450

455

460

ttg cgg tta ccc tat cct ttt tct aac aag caa gtg gat aaa tac ctt 1500

Leu Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu

465

470

475

cta aga cct ttg gga cct cat gga tta ctt tcc aaa tct gtc caa ctc 1548

Leu Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu

480 485 490 495

aat ggt cta act cta aag atg gtg gat gat caa acc ttg cca cct tta 1596

Asn Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu

500 505 510

atg gaa aaa cct ctc cgg cca gga agt tca ctg ggc ttg cca gct ttc 1644

Met Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe

515 520 525

tca tat agt ttt ttt gtg ata aga aat gcc aaa gtt gct gct tgc atc 1692

Ser Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile

530 535 540

tgaaaataaa atatactagt cctgacactg 1722

<210> 90

<211> 543

<212> PRT

<213> Homo sapiens

<400> 90

Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu

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Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro

20 25 30

Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro

35

40

45

Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn

50

55

60

Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu

65

70

75

80

Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly

85

90

95

Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe

100

105

110

Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys

115

120

125

Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp

130

135

140

Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe

145

150

155

160

Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe

165

170

175

Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu

180

185

190

Gly Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu

195

200

205

Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn

210

215

220

Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser

225

230

235

240

Gln Leu Gly Glu Asp Phe Ile Gln Leu His Lys Leu Leu Arg Lys Ser

245

250

255

Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg

260

265

270

Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu

275

280

285

~~Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr~~

290

295

300

Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile

305

310

315

320

Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly

325

330

335

Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala His Gly Gly Gly Ala
340 345 350

Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys
355 360 365

Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val
370 375 380

Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro
385 390 395 400

Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr
405 410 415

Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg
420 425 430

Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly
435 440 445

Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu
450 455 460

Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu
465 470 475 480

Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn
485 490 495

Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met

500

505

510

Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser

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Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile

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<222> (46)..(1737)

<400> 91

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Ser Thr Ala Val Lys Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro

5

10

15

20

gtc att ctt ctg ctt ctg gga gct cac ccg tca cca ctg tgc ttt ttc 153

Val Ile Leu Leu Leu Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe

25

30

35

agt gcg gga ccg gca acc gta gct gct gcc gac cgg tcc aaa tgg cac 201

Ser Ala Gly Pro Ala Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His

40

45

50

att ccg ata ccg tgc ggg aaa aat tat ttt agt ttt gga aag atc ctc 249

Ile Pro Ile Pro Ser Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu

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ttc aga aat acc act atc ttc ctg aag ttt gat gga gaa cct tgt gac 297

Phe Arg Asn Thr Thr Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp

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75

80

ctg tct ttg aat ata acc tgg tat ctg aaa agc gct gat tgt tac aat 345

Leu Ser Leu Asn Ile Thr Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn

85

90

95

100

~~gaa atc tat aac ttc aag gca gaa gaa gta gag ttg tat ttg gaa aaa 393~~

Glu Ile Tyr Asn Phe Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys

105

110

115

ctt aag gaa aaa aga ggc ttg tct ggg aaa tat caa aca tca tca aaa 441

Leu Lys Glu Lys Arg Gly Leu Ser Gly Lys Tyr Gln Thr Ser Ser Lys

120

125

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ttg ttc cag aac tgc agt gaa ctc ttt aaa aca cag acc ttt tct gga 489

Leu Phe Gln Asn Cys Ser Glu Leu Phe Lys Thr Gln Thr Phe Ser Gly

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gat ttt atg cat cga ctg cct ctt tta gga gaa aaa cag gag gct aag 537

Asp Phe Met His Arg Leu Pro Leu Leu Gly Glu Lys Gln Glu Ala Lys

150

155

160

gag aat gga aca aac ctt acc ttt att gga gac aaa acc gca atg cat 585

Glu Asn Gly Thr Asn Leu Thr Phe Ile Gly Asp Lys Thr Ala Met His

165

170

175

180

gaa cca ttg caa act tgg caa gat gca cca tac att ttt att gta cat 633

Glu Pro Leu Gln Thr Trp Gln Asp Ala Pro Tyr Ile Phe Ile Val His

185

190

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att ggc att tca tcc tca aag gaa tca tca aaa gaa aat tca ctg agt 681

Ile Gly Ile Ser Ser Ser Lys Glu Ser Ser Lys Glu Asn Ser Leu Ser

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aat ctt ttt acc atg act gtt gaa gtg aag ggt ccc tat gaa tac ctc 729

~~Asn Leu Phe Thr Met Thr Val Glu Val Lys Gly Pro Tyr Glu Tyr Leu~~

215

220

225

aca ctt gaa gac tat ccc ttg atg att ttt ttc atg gtg atg tgt att 777

Thr Leu Glu Asp Tyr Pro Leu Met Ile Phe Phe Met Val Met Cys Ile

230

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gta tat gtc ctg ttt ggt gtt ctg tgg ctg gca tgg tct gcc tgc tac 825

Val Tyr Val Leu Phe Gly Val Leu Trp Leu Ala Trp Ser Ala Cys Tyr

245

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255

260

tgg aga gat ctc ctg aga att cag ttt tgg att ggt gct gtc atc ttc 873

Trp Arg Asp Leu Leu Arg Ile Gln Phe Trp Ile Gly Ala Val Ile Phe

265

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275

ctg gga atg ctt gag aaa gct gtc ttc tat gcg gaa ttt cag aat atc 921

Leu Gly Met Leu Glu Lys Ala Val Phe Tyr Ala Glu Phe Gln Asn Ile

280

285

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cga tac aaa gga gaa tct gtc cag ggt gct ttg atc ctt gca gag ctg 969

Arg Tyr Lys Gly Glu Ser Val Gln Gly Ala Leu Ile Leu Ala Glu Leu

295

300

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ctt tca gca gtg aaa cgc tca ctg gct cga acc ctg gtc atc ata gtc 1017

Leu Ser Ala Val Lys Arg Ser Leu Ala Arg Thr Leu Val Ile Ile Val

310

315

320

agt ctg gga tat ggc atc gtc aag cca cgc ctt gga gtc act ctt cat 1065

Ser Leu Gly Tyr Gly Ile Val Lys Pro Arg Leu Gly Val Thr Leu His

325

330

335

340

aag gtt gta gta gca gga gcc ctc tat ctt ttg ttc tct ggc atg gaa 1113

Lys Val Val Val Ala Gly Ala Leu Tyr Leu Leu Phe Ser Gly Met Glu

345

350

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ggg gtc ctc aga gtt act ggg gcc cag act gat ctt gct tcc ttg gcc 1161

Gly Val Leu Arg Val Thr Gly Ala Gln Thr Asp Leu Ala Ser Leu Ala

360

365

370

ttt atc ccc ttg gct ttc cta gac act gcc ttg tgc tgg tgg ata ttt 1209

Phe Ile Pro Leu Ala Phe Leu Asp Thr Ala Leu Cys Trp Trp Ile Phe

375

380

385

att agc ctg act caa aca atg aag cta tta aaa ctt cgg agg aac att 1257

Ile Ser Leu Thr Gln Thr Met Lys Leu Leu Lys Leu Arg Arg Asn Ile

390

395

400

gta aaa ctc tct ttg tat cgg cat ttc acc aac acg ctt att ttg gca 1305

Val Lys Leu Ser Leu Tyr Arg His Phe Thr Asn Thr Leu Ile Leu Ala

405

410

415

420

gtg gca gca tcc att gtg ttt atc atc tgg aca acc atg aag ttc aga 1353

Val Ala Ala Ser Ile Val Phe Ile Ile Trp Thr Thr Met Lys Phe Arg

425

430

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ata gtg aca tgt cag tcg gac tgg cgg gag ctg tgg gta gac gat gcc 1401

Ile Val Thr Cys Gln Ser Asp Trp Arg Glu Leu Trp Val Asp Asp Ala

440

445

450

atc tgg cgc ttg ctg ttc tcc atg atc ctc ttt gtc atc atg gtt ctc 1449

Ile Trp Arg Leu Leu Phe Ser Met Ile Leu Phe Val Ile Met Val Leu

455

460

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tgg cga cca tct gca aac aac cag agg ttt gcc ttt tca cca ttg tct 1497

Trp Arg Pro Ser Ala Asn Asn Gln Arg Phe Ala Phe Ser Pro Leu Ser

470

475

480

gag gaa gag gag gag gat gaa caa aag gag cct atg ctg aaa gaa agc 1545
 Glu Glu Glu Glu Glu Asp Glu Gln Lys Glu Pro Met Leu Lys Glu Ser
 485 490 495 500

ttt gaa gga atg aaa atg aga agt acc aaa caa gaa ccc aat gga aat 1593
 Phe Glu Gly Met Lys Met Arg Ser Thr Lys Gln Glu Pro Asn Gly Asn
 505 510 515

agt aaa gtt aac aaa gca cag gaa gat gat tcg aag tgg gta gaa gag 1641
 Ser Lys Val Asn Lys Ala Gln Glu Asp Asp Ser Lys Trp Val Glu Glu
 520 525 530

aat gtt cct tct tct gtg aca gat gta gca ctt cca gcc ctt ctg gat 1689
 Asn Val Pro Ser Ser Val Thr Asp Val Ala Leu Pro Ala Leu Leu Asp
 535 540 545

tca gat gag gaa cga atg atc aca cac ttt gaa agg tcc aaa atg gag 1737
 Ser Asp Glu Glu Arg Met Ile Thr His Phe Glu Arg Ser Lys Met Glu
 550 555 560

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aacaagtcca taagatgaga aaaatctacg agcttcttat ttacaacact gctgccccct 1977

ttcctcccag actctgacat ggatgttcat gcaacttaag tgtgttgttc ctgaactttc 2037

tgtaatgttt catttttta atctgacaaa ctaaaaagtt taacgtcttc taaaagattg 2097

tcatcaacac cataatatgt aatctccagg agcaactgcc tgtaattttt atttatattag 2157

ggagttacat aggtgatggg ggaaattggt aactaccttt cattttcctg ggaagtcaag 2217

gttacatctt gcagaggttg ttttgagaaa aaagggccct tctgagttaa ggagccatag 2277

ttctatcaat gatc 2291

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<212> PRT

<213> Homo sapiens

<400> 92

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Gln Val Leu Pro Val Ile Leu Leu Leu Leu Gly Ala His Pro Ser Pro

20 25 30

Leu Ser Phe Phe Ser Ala Gly Pro Ala Thr Val Ala Ala Ala Asp Arg

35 40 45

Ser Lys Trp His Ile Pro Ile Pro Ser Gly Lys Asn Tyr Phe Ser Phe

50 55 60

Gly Lys Ile Leu Phe Arg Asn Thr Thr Ile Phe Leu Lys Phe Asp Gly
65 70 75 80

Glu Pro Cys Asp Leu Ser Leu Asn Ile Thr Trp Tyr Leu Lys Ser Ala
85 90 95

Asp Cys Tyr Asn Glu Ile Tyr Asn Phe Lys Ala Glu Glu Val Glu Leu
100 105 110

Tyr Leu Glu Lys Leu Lys Glu Lys Arg Gly Leu Ser Gly Lys Tyr Gln
115 120 125

Thr Ser Ser Lys Leu Phe Gln Asn Cys Ser Glu Leu Phe Lys Thr Gln
130 135 140

Thr Phe Ser Gly Asp Phe Met His Arg Leu Pro Leu Leu Gly Glu Lys
145 150 155 160

Gln Glu Ala Lys Glu Asn Gly Thr Asn Leu Thr Phe Ile Gly Asp Lys
165 170 175

Thr Ala Met His Glu Pro Leu Gln Thr Trp Gln Asp Ala Pro Tyr Ile
180 185 190

Phe Ile Val His Ile Gly Ile Ser Ser Ser Lys Glu Ser Ser Lys Glu
195 200 205

Asn Ser Leu Ser Asn Leu Phe Thr Met Thr Val Glu Val Lys Gly Pro

210

215

220

Tyr Glu Tyr Leu Thr Leu Glu Asp Tyr Pro Leu Met Ile Phe Phe Met

225

230

235

240

Val Met Cys Ile Val Tyr Val Leu Phe Gly Val Leu Trp Leu Ala Trp

245

250

255

Ser Ala Cys Tyr Trp Arg Asp Leu Leu Arg Ile Gln Phe Trp Ile Gly

260

265

270

Ala Val Ile Phe Leu Gly Met Leu Glu Lys Ala Val Phe Tyr Ala Glu

275

280

285

Phe Gln Asn Ile Arg Tyr Lys Gly Glu Ser Val Gln Gly Ala Leu Ile

290

295

300

Leu Ala Glu Leu Leu Ser Ala Val Lys Arg Ser Leu Ala Arg Thr Leu

305

310

315

320

~~Val Ile Ile Val Ser Leu Gly Tyr Gly Ile Val Lys Pro Arg Leu Gly~~

325

330

335

Val Thr Leu His Lys Val Val Val Ala Gly Ala Leu Tyr Leu Leu Phe

340

345

350

Ser Gly Met Glu Gly Val Leu Arg Val Thr Gly Ala Gln Thr Asp Leu

355

360

365

Ala Ser Leu Ala Phe Ile Pro Leu Ala Phe Leu Asp Thr Ala Leu Cys
370 375 380

Trp Trp Ile Phe Ile Ser Leu Thr Gln Thr Met Lys Leu Leu Lys Leu
385 390 395 400

Arg Arg Asn Ile Val Lys Leu Ser Leu Tyr Arg His Phe Thr Asn Thr
405 410 415

Leu Ile Leu Ala Val Ala Ala Ser Ile Val Phe Ile Ile Trp Thr Thr
420 425 430

Met Lys Phe Arg Ile Val Thr Cys Gln Ser Asp Trp Arg Glu Leu Trp
435 440 445

Val Asp Asp Ala Ile Trp Arg Leu Leu Phe Ser Met Ile Leu Phe Val
450 455 460

Ile Met Val Leu Trp Arg Pro Ser Ala Asn Asn Gln Arg Phe Ala Phe
465 470 475 480

Ser Pro Leu Ser Glu Glu Glu Glu Glu Asp Glu Gln Lys Glu Pro Met
485 490 495

Leu Lys Glu Ser Phe Glu Gly Met Lys Met Arg Ser Thr Lys Gln Glu
500 505 510

Pro Asn Gly Asn Ser Lys Val Asn Lys Ala Gln Glu Asp Asp Ser Lys
515 520 525

Trp Val Glu Glu Asn Val Pro Ser Ser Val Thr Asp Val Ala Leu Pro

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535

540

Ala Leu Leu Asp Ser Asp Glu Glu Arg Met Ile Thr His Phe Glu Arg

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550

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Ser Lys Met Glu

<210> 93

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cgggcgagcg aggctgcggg ccggccgctg cccttcccca cactccccgc cgagaagcct 180

cgctcggcgc ccaac atg gcg ggt ggg cgc tgc ggc ccg cag cta acg gcg 231

Met Ala Gly Gly Arg Cys Gly Pro Gln Leu Thr Ala

1

5

10

ctc ctg gcc gcc tgg atc gcg gct gtg gcg gcg acg gca ggc ccc gag 279

Leu Leu Ala Ala Trp Ile Ala Ala Val Ala Ala Thr Ala Gly Pro Glu

15

20

25

gag gcc gcg ctg ccg ccg gag cag agc cgg gtc cag ccc atg acc gcc 327

Glu Ala Ala Leu Pro Pro Glu Gln Ser Arg Val Gln Pro Met Thr Ala

30

35

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tcc aac tgg acg ctg gtg atg gag ggc gag tgg atg ctg aaa ttt tac 375

Ser Asn Trp Thr Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr

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gcc cca tgg tgt cca tcc tgc cag cag act gat tca gaa tgg gag gct 423

Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu Ala

65

70

75

ttt gca aag aat ggt gaa ata ctt cag atc agt gtg ggg aag gta gat 471

Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys Val Asp

80

85

90

gtc att caa gaa cca ggt ttg agt ggc cgc ttc ttt gtc acc act ctc 519

Val Ile Gln Glu Pro Gly Leu Ser Gly Arg Phe Phe Val Thr Thr Leu

95

100

105

cca gca ttt ttt cat gca aag gat ggg ata ttc cgc cgt tat cgt ggc 567

Pro Ala Phe Phe His Ala Lys Asp Gly Ile Phe Arg Arg Tyr Arg Gly

110

115

120

cca gga atc ttc gaa gac ctg cag aat tat atc tta gag aag aaa tgg 615

Pro Gly Ile Phe Glu Asp Leu Gln Asn Tyr Ile Leu Glu Lys Lys Trp

125 130 135 140

caa tca gtc gag cct ctg act ggc tgg aaa tcc cca gct tct cta acg 663

Gln Ser Val Glu Pro Leu Thr Gly Trp Lys Ser Pro Ala Ser Leu Thr

145 150 155

atg tct gga atg gct ggt ctt ttt agc atc tct ggc aag ata tgg cat 711

Met Ser Gly Met Ala Gly Leu Phe Ser Ile Ser Gly Lys Ile Trp His

160 165 170

ctt cac aac tat ttc aca gtg act ctt gga att cct gct tgg tgt tct 759

Leu His Asn Tyr Phe Thr Val Thr Leu Gly Ile Pro Ala Trp Cys Ser

175 180 185

tat gtg ttt ttc gtc ata gcc acc ttg gtt ttt ggc ctt ttt atg ggt 807

Tyr Val Phe Phe Val Ile Ala Thr Leu Val Phe Gly Leu Phe Met Gly

190 195 200

ctg gtc ttg gtg gta ata tca gaa tgt ttc tat gtg cca ctt cca agg 855

Leu Val Leu Val Val Ile Ser Glu Cys Phe Tyr Val Pro Leu Pro Arg

205 210 215 220

cat tta tct gag cgt tct gag cag aat cgg aga tca gag gag gct cat 903

His Leu Ser Glu Arg Ser Glu Gln Asn Arg Arg Ser Glu Glu Ala His

225 230 235

aga gct gaa cag ttg cag gat gcg gag gag gaa aaa gat gat tca aat 951
 Arg Ala Glu Gln Leu Gln Asp Ala Glu Glu Glu Lys Asp Asp Ser Asn
 240 245 250

gaa gaa gaa aac aaa gac agc ctt gta gat gat gaa gaa gag aaa gaa 999
 Glu Glu Glu Asn Lys Asp Ser Leu Val Asp Asp Glu Glu Glu Lys Glu
 255 260 265

gat ctt ggc gat gag gat gaa gca gag gaa gaa gag gag gag gac aac 1047
 Asp Leu Gly Asp Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Asp Asn
 270 275 280

ttg gct gct ggt gtg gat gag gag aga agt gag gcc aat gat cag ggg 1095
 Leu Ala Ala Gly Val Asp Glu Glu Arg Ser Glu Ala Asn Asp Gln Gly
 285 290 295 300

ccc cca gga gag gac ggt gtg acc cgg gag gaa gta gag cct gag gag 1143
 Pro Pro Gly Glu Asp Gly Val Thr Arg Glu Glu Val Glu Pro Glu Glu
 305 310 315

~~gct gaa gaa ggc atc tct gag caa ccc tgc cca gct gac aca gag gtg 1191~~

Ala Glu Glu Gly Ile Ser Glu Gln Pro Cys Pro Ala Asp Thr Glu Val
 320 325 330

gtg gaa gac tcc ttg agg cag cgt aaa agt cag cat gct gac aag gga 1239
 Val Glu Asp Ser Leu Arg Gln Arg Lys Ser Gln His Ala Asp Lys Gly
 335 340 345

ctg tagatttaat gatgcgtttt caagaatata caccaaaaca atatgtcagc 1292

Leu

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ttaaaagatg ctctctagtc atttggcttc atggcagtaa gcctcatgta tactaaggag 1412

agtcttccag gtgtgacaat caggatatag aaaaacaaac gtagtggttg gatctgtttg 1472

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ccattcccag tcctaatacag caccttccag agacaaggct gcaggccctg tgaaatgaaa 1592

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gtcatcccag ccctctgaat ctctgtgct atgttttatt tcttaccttt aatttttcca 1832

~~gcatttccac catgggcatt caggctctcc acactcttca ctattatctc ttggtcagag 1892~~

gactccaata acagccaggt ttacatgaac tgtgtttgtt cattctgacc taaggggttt 1952

agataatcag taaccataac ccctgaagct gtgactgcc aacatctcaa atgaaatgtt 2012

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2080

<210> 94

<211> 349

<212> PRT

<213> Homo sapiens

<400> 94

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Trp Ile Ala Ala Val Ala Ala Thr Ala Gly Pro Glu Glu Ala Ala Leu

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30

Pro Pro Glu Gln Ser Arg Val Gln Pro Met Thr Ala Ser Asn Trp Thr

35

40

45

Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr Ala Pro Trp Cys

50

55

60

Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu Ala Phe Ala Lys Asn

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70

75

80

Gly Glu Ile Leu Gln Ile Ser Val Gly Lys Val Asp Val Ile Gln Glu

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90

95

Pro Gly Leu Ser Gly Arg Phe Phe Val Thr Thr Leu Pro Ala Phe Phe

100

105

110

His Ala Lys Asp Gly Ile Phe Arg Arg Tyr Arg Gly Pro Gly Ile Phe
115 120 125

Glu Asp Leu Gln Asn Tyr Ile Leu Glu Lys Lys Trp Gln Ser Val Glu
130 135 140

Pro Leu Thr Gly Trp Lys Ser Pro Ala Ser Leu Thr Met Ser Gly Met
145 150 155 160

Ala Gly Leu Phe Ser Ile Ser Gly Lys Ile Trp His Leu His Asn Tyr
165 170 175

Phe Thr Val Thr Leu Gly Ile Pro Ala Trp Cys Ser Tyr Val Phe Phe
180 185 190

Val Ile Ala Thr Leu Val Phe Gly Leu Phe Met Gly Leu Val Leu Val
195 200 205

Val Ile Ser Glu Cys Phe Tyr Val Pro Leu Pro Arg His Leu Ser Glu
210 215 220

Arg Ser Glu Gln Asn Arg Arg Ser Glu Glu Ala His Arg Ala Glu Gln
225 230 235 240

Leu Gln Asp Ala Glu Glu Glu Lys Asp Asp Ser Asn Glu Glu Glu Asn
245 250 255

Lys Asp Ser Leu Val Asp Asp Glu Glu Glu Lys Glu Asp Leu Gly Asp
260 265 270

Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Asp Asn Leu Ala Ala Gly
 275 280 285

Val Asp Glu Glu Arg Ser Glu Ala Asn Asp Gln Gly Pro Pro Gly Glu
 290 295 300

Asp Gly Val Thr Arg Glu Glu Val Glu Pro Glu Glu Ala Glu Glu Gly
 305 310 315 320

Ile Ser Glu Gln Pro Cys Pro Ala Asp Thr Glu Val Val Glu Asp Ser
 325 330 335

Leu Arg Gln Arg Lys Ser Gln His Ala Asp Lys Gly Leu
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<210> 95

<211> 2185

<212> DNA

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<222> (73)..(696)

<400> 95

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Met Leu Gly Leu Leu Val Ala Leu Leu Ala Leu Gly Leu

1 5 10

gct gtc ttt gcg ctg ctg ggc gtc tgg tac ctg gtg cgc ctt ccg tgc 159

Ala Val Phe Ala Leu Leu Gly Val Trp Tyr Leu Val Arg Leu Pro Cys

15 20 25

gcc gtg ctg cgc gcg cgc ctg ctg cag ccg cgc gtc cgt gac ctg cta 207

Ala Val Leu Arg Ala Arg Leu Leu Gln Pro Arg Val Arg Asp Leu Leu

30 35 40 45

gct gag cag cgc ttc ccg ggc cgc gtg ctg ccc tcg gac ttg gac ctg 255

Ala Glu Gln Arg Phe Pro Gly Arg Val Leu Pro Ser Asp Leu Asp Leu

50 55 60

ctg ttg cac atg aac aac gcg cgc tac ctg cgc gag gcc gac ttt gcg 303

Leu Leu His Met Asn Asn Ala Arg Tyr Leu Arg Glu Ala Asp Phe Ala

65 70 75

~~cgc-gtc-gcg-cac-ctg-acc-cgc-tgc-ggg-gtg-ctc-ggg-gcg-ctg-agg-gag~~ 351

Arg Val Ala His Leu Thr Arg Cys Gly Val Leu Gly Ala Leu Arg Glu

80 85 90

ttg cgg gcg cac acg gtg ctg gcg gcc tcg tgc gcg cgc cac cgc cgc 399

Leu Arg Ala His Thr Val Leu Ala Ala Ser Cys Ala Arg His Arg Arg

95 100 105

tcg ctg cgc ctg ctg gag ccc ttc gag gtg cgc acc cgc ctg ctg ggc 447

Ser Leu Arg Leu Leu Glu Pro Phe Glu Val Arg Thr Arg Leu Leu Gly

110 115 120 125

tgg gac gac cgc gcg ttc tac ctg gag gcg cgc ttt gtc agc ctg cgg 495

Trp Asp Asp Arg Ala Phe Tyr Leu Glu Ala Arg Phe Val Ser Leu Arg

130 135 140

gac ggt ttc gtg tgc gcg ctg ctg cgc ttc cgg cag cac ctg ctg ggc 543

Asp Gly Phe Val Cys Ala Leu Leu Arg Phe Arg Gln His Leu Leu Gly

145 150 155

acc tca ccc gag cgc gtc gtg cag cac ctg tgc cag cgc agg gtg gag 591

Thr Ser Pro Glu Arg Val Val Gln His Leu Cys Gln Arg Arg Val Glu

160 165 170

ccc cct gag ctg ccc gct gat ctg cag cac tgg atc tcc tac aac gag 639

Pro Pro Glu Leu Pro Ala Asp Leu Gln His Trp Ile Ser Tyr Asn Glu

175 180 185

gcc agc agc cag ctg ctc cgc atg gag agt ggg ctc agt gat gtc acc 687

~~Ala Ser Ser Gln Leu Leu Arg Met Glu Ser Gly Leu Ser Asp Val Thr~~

190 195 200 205

aag gac cag tgaccgccac cttcacaccg tctgccctgg ccaccatcct 736

Lys Asp Gln

gggcctgggg gctgcccaca gatgggcagt ctcagccata ctctgttcca gctggagtag 796

cctcctgacc agcctggccc accctgctcc acccaactggg cccccccagt tattgatacc 856

cctctgtgct gggctccacg ctaggcagaa ggaggagtgg cattggcatc ctgaccacgc 916

tctgccctca aggtggggat ggatgggcaa aggagagtcc tgcctggccc tacgatgagg 976

ccactcatgt gggcctaggt aggggaggat ggtgcctgga gcagagggac ccacaagtgc 1036

ctcccagacc tagatcctgg ctcggaccac tgcaagggcc gaggcagggc cagaccagag 1096

catcctgggt acaggcctgg gctctccagg gtctgggcct gattcaggtg cagtgggcac 1156

tcctgaaggg tcagagcggc atctgccagg cagccccctt ggcttccgct gaggtggttg 1216

caggcctggg gcagagcctg ggtggtcaga ggccggggct agaggcagat ggaaggagg 1276

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ctactaggac actggctggg gccaccccct cctgcctaatt gcctcacctt acagctgggg 1816

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aggctccagc tgatgccctc agctcccaga gaggggggtgc cccatctagc tgggtgcagg 1936

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tgcacatcca gaactgcctc ctggccgtg cctccaggaa gccaccttg agccagagtc 2056

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tttcattgc 2185

<210> 96

<211> 208

<212> PRT

<213> Homo sapiens

<400> 96

Met Leu Gly Leu Leu Val Ala Leu Leu Ala Leu Gly Leu Ala Val Phe

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Ala Leu Leu Gly Val Trp Tyr Leu Val Arg Leu Pro Cys Ala Val Leu

20

25

30

Arg Ala Arg Leu Leu Gln Pro Arg Val Arg Asp Leu Leu Ala Glu Gln

35

40

45

Arg Phe Pro Gly Arg Val Leu Pro Ser Asp Leu Asp Leu Leu Leu His

50

55

60

Met Asn Asn Ala Arg Tyr Leu Arg Glu Ala Asp Phe Ala Arg Val Ala

65

70

75

80

His Leu Thr Arg Cys Gly Val Leu Gly Ala Leu Arg Glu Leu Arg Ala

85

90

95

His Thr Val Leu Ala Ala Ser Cys Ala Arg His Arg Arg Ser Leu Arg

100

105

110

Leu Leu Glu Pro Phe Glu Val Arg Thr Arg Leu Leu Gly Trp Asp Asp

115

120

125

Arg Ala Phe Tyr Leu Glu Ala Arg Phe Val Ser Leu Arg Asp Gly Phe

130

135

140

Val Cys Ala Leu Leu Arg Phe Arg Gln His Leu Leu Gly Thr Ser Pro

145

150

155

160

Glu Arg Val Val Gln His Leu Cys Gln Arg Arg Val Glu Pro Pro Glu

165

170

175

Leu Pro Ala Asp Leu Gln His Trp Ile Ser Tyr Asn Glu Ala Ser Ser

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185

190

Gln Leu Leu Arg Met Glu Ser Gly Leu Ser Asp Val Thr Lys Asp Gln

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<210> 97

<211> 1627

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (251)..(1300)

<400> 97

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gaacccaacg gcagacaggt cctagtgcc atcagatacc cgcggccggg actcggagct 180

gtggggtgtg gggaggcgga ggcaccaact aagagcggcc tagcatcgca aagccgccct 240

cggggcgctc atg gcg gga cgc ctc ctg gga aag gct ttg gcc gcg gtg 289

Met Ala Gly Arg Leu Leu Gly Lys Ala Leu Ala Ala Val

1

5

10

tct ctc tct ctg gcc ttg gcc tct gtg act atc agg tcc tcg cgc tgc 337

Ser Leu Ser Leu Ala Leu Ala Ser Val Thr Ile Arg Ser Ser Arg Cys

15

20

25

cgc ggc atc cag gcg ttc aga aac tcg ttt tca tct tct tgg ttt cat 385

Arg Gly Ile Gln Ala Phe Arg Asn Ser Phe Ser Ser Ser Trp Phe His

30

35

40

45

ctt aat acc aac gtc atg tct ggt tct aat ggt tcc aaa gaa aat tct 433

Leu Asn Thr Asn Val Met Ser Gly Ser Asn Gly Ser Lys Glu Asn Ser

50

55

60

cac aat aag gct cgg acg tct cct tac cca ggt tca aaa gtt gaa cga 481

His Asn Lys Ala Arg Thr Ser Pro Tyr Pro Gly Ser Lys Val Glu Arg

65

70

75

agc cag gtt cct aat gag aaa gtg ggc tgg ctt gtt gag tgg caa gac 529

Ser Gln Val Pro Asn Glu Lys Val Gly Trp Leu Val Glu Trp Gln Asp

80

85

90

~~tat aag cct gtg gaa tac act gca gtc tct gtc ttg gct gga ccc agg 577~~

Tyr Lys Pro Val Glu Tyr Thr Ala Val Ser Val Leu Ala Gly Pro Arg

95

100

105

tgg gca gat cct cag atc agt gaa agt aat ttt tct ccc aag ttt aac 625

Trp Ala Asp Pro Gln Ile Ser Glu Ser Asn Phe Ser Pro Lys Phe Asn

110

115

120

125

gaa aag gat ggg cat gtt gag aga aag agc aag aat ggc ctg tat gag 673

Glu Lys Asp Gly His Val Glu Arg Lys Ser Lys Asn Gly Leu Tyr Glu

130

135

140

att gaa aat gga aga ccg aga aat cct gca gga cgg act gga ctg gtg 721

Ile Glu Asn Gly Arg Pro Arg Asn Pro Ala Gly Arg Thr Gly Leu Val

145

150

155

ggc cgg ggg ctt ttg ggg cga tgg ggc cca aat cac gct gca gat ccc 769

Gly Arg Gly Leu Leu Gly Arg Trp Gly Pro Asn His Ala Ala Asp Pro

160

165

170

att ata acc aga tgg aaa agg gat agc agt gga aat aaa atc atg cat 817

Ile Ile Thr Arg Trp Lys Arg Asp Ser Ser Gly Asn Lys Ile Met His

175

180

185

cct gtt tct ggg aag cat atc tta caa ttt gtt gca ata aaa agg aaa 865

Pro Val Ser Gly Lys His Ile Leu Gln Phe Val Ala Ile Lys Arg Lys

190

195

200

205

gac tgt gga gaa tgg gca atc cca ggg ggg atg gtg gat cca gga gag 913

Asp Cys Gly Glu Trp Ala Ile Pro Gly Gly Met Val Asp Pro Gly Glu

210

215

220

aag att agt gcc aca ctg aaa aga gaa ttt ggt gag gaa gct ctc aac 961

Lys Ile Ser Ala Thr Leu Lys Arg Glu Phe Gly Glu Glu Ala Leu Asn

225

230

235

tcc tta cag aaa acc agt gct gag aag aga gaa ata gag gaa aag ttg 1009

Ser Leu Gln Lys Thr Ser Ala Glu Lys Arg Glu Ile Glu Glu Lys Leu

240

245

250

cac aaa ctc ttc agc caa gac cac cta gtg ata tat aag gga tat gtt 1057

His Lys Leu Phe Ser Gln Asp His Leu Val Ile Tyr Lys Gly Tyr Val

255

260

265

gat gat cct cga aac act gat aat gca tgg atg gag aca gaa gct gtg 1105

Asp Asp Pro Arg Asn Thr Asp Asn Ala Trp Met Glu Thr Glu Ala Val

270

275

280

285

aac tac cat gac gaa aca ggt gtg ata atg gat aat ctt atg cta gaa 1153

Asn Tyr His Asp Glu Thr Gly Val Ile Met Asp Asn Leu Met Leu Glu

290

295

300

gct gga gat gat gct gga aaa gtg aaa tgg gtg gac atc aat gat aaa 1201

Ala Gly Asp Asp Ala Gly Lys Val Lys Trp Val Asp Ile Asn Asp Lys

305

310

315

ctg aag ctt tat gcc agt cac tct caa ttc atc aaa ctt gtg gct gag 1249

Leu Lys Leu Tyr Ala Ser His Ser Gln Phe Ile Lys Leu Val Ala Glu

320

325

330

aaa cga gat gca cac tgg agc gag gac tct gaa gct gac tgc cat gcg 1297

Lys Arg Asp Ala His Trp Ser Glu Asp Ser Glu Ala Asp Cys His Ala

335

340

345

ttg tagctgatgg tctccgtgta agccaaaggc ccacagagga gcatatactg 1350

Leu

350

aaaagaaggc agtatcacag aatttatact ataaaaaggg cagggtaggc cacttggcct 1410

atttactttc aaaacaactt gcatttagag tgtttcgcat cagaataaca tgagtaagat 1470

gaactggaac acaaaatttt cagctctttg gtcaaaagga atataagtaa tcatattttg 1530

tatgtattcg atttaagcat ggcttaaatt aaatttaaac aactaatgct ctttgaagaa 1590

tcataatcag aataaagata aattcttgat cagctat 1627

<210> 98

<211> 350

<212> PRT

<213> Homo sapiens

<400> 98

Met Ala Gly Arg Leu Leu Gly Lys Ala Leu Ala Ala Val Ser Leu Ser

1

5

10

15

Leu Ala Leu Ala Ser Val Thr Ile Arg Ser Ser Arg Cys Arg Gly Ile

20

25

30

Gln Ala Phe Arg Asn Ser Phe Ser Ser Ser Trp Phe His Leu Asn Thr

35

40

45

Asn Val Met Ser Gly Ser Asn Gly Ser Lys Glu Asn Ser His Asn Lys

50

55

60

Ala Arg Thr Ser Pro Tyr Pro Gly Ser Lys Val Glu Arg Ser Gln Val
65 70 75 80

Pro Asn Glu Lys Val Gly Trp Leu Val Glu Trp Gln Asp Tyr Lys Pro
85 90 95

Val Glu Tyr Thr Ala Val Ser Val Leu Ala Gly Pro Arg Trp Ala Asp
100 105 110

Pro Gln Ile Ser Glu Ser Asn Phe Ser Pro Lys Phe Asn Glu Lys Asp
115 120 125

Gly His Val Glu Arg Lys Ser Lys Asn Gly Leu Tyr Glu Ile Glu Asn
130 135 140

Gly Arg Pro Arg Asn Pro Ala Gly Arg Thr Gly Leu Val Gly Arg Gly
145 150 155 160

Leu Leu Gly Arg Trp Gly Pro Asn His Ala Ala Asp Pro Ile Ile Thr
165 170 175

Arg Trp Lys Arg Asp Ser Ser Gly Asn Lys Ile Met His Pro Val Ser
180 185 190

Gly Lys His Ile Leu Gln Phe Val Ala Ile Lys Arg Lys Asp Cys Gly
195 200 205

Glu Trp Ala Ile Pro Gly Gly Met Val Asp Pro Gly Glu Lys Ile Ser

210

215

220

Ala Thr Leu Lys Arg Glu Phe Gly Glu Glu Ala Leu Asn Ser Leu Gln

225

230

235

240

Lys Thr Ser Ala Glu Lys Arg Glu Ile Glu Glu Lys Leu His Lys Leu

245

250

255

Phe Ser Gln Asp His Leu Val Ile Tyr Lys Gly Tyr Val Asp Asp Pro

260

265

270

Arg Asn Thr Asp Asn Ala Trp Met Glu Thr Glu Ala Val Asn Tyr His

275

280

285

Asp Glu Thr Gly Val Ile Met Asp Asn Leu Met Leu Glu Ala Gly Asp

290

295

300

Asp Ala Gly Lys Val Lys Trp Val Asp Ile Asn Asp Lys Leu Lys Leu

305

310

315

320

~~Tyr Ala Ser His Ser Gln Phe Ile Lys Leu Val Ala Glu Lys Arg Asp~~

325

330

335

Ala His Trp Ser Glu Asp Ser Glu Ala Asp Cys His Ala Leu

340

345

350

<210> 99

<211> 1391

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74)..(589)

<400> 99

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cgcacctact gcc atg gag acg cgg cct cgt ctc ggg gcc acc tgt ttg 109

Met Glu Thr Arg Pro Arg Leu Gly Ala Thr Cys Leu

1

5

10

ctg ggc ttc agt ttc ctg ctc ctc gtc atc tct tct gat gga cat aat 157

Leu Gly Phe Ser Phe Leu Leu Leu Val Ile Ser Ser Asp Gly His Asn

15

20

25

ggg ctt gga aag ggt ttt gga gat cat att cat tgg agg aca ctg gaa 205

Gly Leu Gly Lys Gly Phe Gly Asp His Ile His Trp Arg Thr Leu Glu

30

35

40

gat ggg aag aaa gaa gca gct gcc agt gga ctg ccc ctg atg gtg att 253

Asp Gly Lys Lys Glu Ala Ala Ala Ser Gly Leu Pro Leu Met Val Ile

45

50

55

60

att cat aaa tcc tgg tgt gga gct tgc aaa gct cta aag ccc aaa ttt 301

Ile His Lys Ser Trp Cys Gly Ala Cys Lys Ala Leu Lys Pro Lys Phe

65

70

75

gca gaa tct acg gaa att tca gaa ctc tcc cat aat ttt gtt atg gta 349

Ala Glu Ser Thr Glu Ile Ser Glu Leu Ser His Asn Phe Val Met Val

80

85

90

aat ctt gag gat gaa gag gaa ccc aaa gat gaa gat ttc agc cct gac 397

Asn Leu Glu Asp Glu Glu Glu Pro Lys Asp Glu Asp Phe Ser Pro Asp

95

100

105

ggg ggt tat att cca cga atc ctt ttt ctg gat ccc agt ggc aag gtg 445

Gly Gly Tyr Ile Pro Arg Ile Leu Phe Leu Asp Pro Ser Gly Lys Val

110

115

120

cat cct gaa atc atc aat gag aat gga aac ccc agc tac aag tat ttt 493

His Pro Glu Ile Ile Asn Glu Asn Gly Asn Pro Ser Tyr Lys Tyr Phe

125

130

135

140

tat gtc agt gcc gag caa gtt gtt cag ggg atg aag gaa gct cag gaa 541

Tyr Val Ser Ala Glu Gln Val Val Gln Gly Met Lys Glu Ala Gln Glu

145

150

155

agg ctg acg ggt gat gcc ttc aga aag aaa cat ctt gaa gat gaa ttg 589

Arg Leu Thr Gly Asp Ala Phe Arg Lys Lys His Leu Glu Asp Glu Leu

160

165

170

taacatgaat gtgccccttc ttcatcaga gttagtgttc tggaaggaaa gcagcaggga 649

agggaatatt gaggaatcat ctagaacaat taagccgacc aggaaacctc attcctacct 709

acactggaag gagcgctctc actgtggaag agttctgcta acagaagctg gtctgcatgt 769

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gtgggtgaaag gagactagta gcatcttttc tacaacgtta aaattgcaga agtagcttat 1009

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gcatgcgtgt gcaggactgg ctgtgtgctt ggactcggct ccagggtggaa gcatgctttc 1249

ccttggttact gttggagaaa ctcaaaccct caagccctag gtgtagccat ttgtcaagt 1309

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actttaataa aactttaaaa gg

1391

<210> 100

<211> 172

<212> PRT

<213> Homo sapiens

<400> 100

Met Glu Thr Arg Pro Arg Leu Gly Ala Thr Cys Leu Leu Gly Phe Ser

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Phe Leu Leu Leu Val Ile Ser Ser Asp Gly His Asn Gly Leu Gly Lys

20 25 30

Gly Phe Gly Asp His Ile His Trp Arg Thr Leu Glu Asp Gly Lys Lys

35 40 45

Glu Ala Ala Ala Ser Gly Leu Pro Leu Met Val Ile Ile His Lys Ser

50 55 60

Trp Cys Gly Ala Cys Lys Ala Leu Lys Pro Lys Phe Ala Glu Ser Thr

65 70 75 80

Glu Ile Ser Glu Leu Ser His Asn Phe Val Met Val Asn Leu Glu Asp

85 90 95

~~Glu Glu Glu Pro Lys Asp Glu Asp Phe Ser Pro Asp Gly Gly Tyr Ile~~

100 105 110

Pro Arg Ile Leu Phe Leu Asp Pro Ser Gly Lys Val His Pro Glu Ile

115 120 125

Ile Asn Glu Asn Gly Asn Pro Ser Tyr Lys Tyr Phe Tyr Val Ser Ala

130 135 140

Glu Gln Val Val Gln Gly Met Lys Glu Ala Gln Glu Arg Leu Thr Gly
 145 150 155 160

Asp Ala Phe Arg Lys Lys His Leu Glu Asp Glu Leu
 165 170

<210> 101

<211> 2547

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (166)..(939)

<400> 101

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cgacaaacgt ggtctgagaa cagcggagcg cggaaaccgc ggagc atg act cct ccg 177

Met Thr Pro Pro

1

aag ctg cga gcg tcg ctg tcg ccg tcg ctg ctg ctg ctg agt ggt 225

Lys Leu Arg Ala Ser Leu Ser Pro Ser Leu Leu Leu Leu Ser Gly

5

10

15

20

tgc ctc ctc gcg gct gct cgg agg gag aaa ggg gcg gct agc aac gtg 273

Cys Leu Leu Ala Ala Ala Arg Arg Glu Lys Gly Ala Ala Ser Asn Val

25

30

35

gcg gag ccg gtc ccc ggg ccc act ggc ggc tcc tcg ggt cgc ttc ctc 321

Ala Glu Pro Val Pro Gly Pro Thr Gly Gly Ser Ser Gly Arg Phe Leu

40

45

50

agc ccc gag cag cac gcg tgc agc tgg cag ctc ctg ctg ccc gcc ccg 369

Ser Pro Glu Gln His Ala Cys Ser Trp Gln Leu Leu Leu Pro Ala Pro

55

60

65

gag gcc gca gcg ggc agc gag ctg gcg ctg cgc tgc cag agc ccg gac 417

Glu Ala Ala Ala Gly Ser Glu Leu Ala Leu Arg Cys Gln Ser Pro Asp

70

75

80

ggg gcg cgc cac cag tgc gcc tac cgc ggg cat ccg gag cgc tgc gca 465

Gly Ala Arg His Gln Cys Ala Tyr Arg Gly His Pro Glu Arg Cys Ala

85

90

95

100

~~gcc tac gcc gct cgc cgc gcg cac ttc tgg aag cag gtg ctg gga ggg 513~~

Ala Tyr Ala Ala Arg Arg Ala His Phe Trp Lys Gln Val Leu Gly Gly

105

110

115

ctg cgc aag aag cgg agg ccc tgt cac gac ccc gcg ccg ctc cag gcc 561

Leu Arg Lys Lys Arg Arg Pro Cys His Asp Pro Ala Pro Leu Gln Ala

120

125

130

cgc ttg tgc gcg ggc aag aag ggc cac ggc gcc gag ctg cgg cta gtg 609

Arg Leu Cys Ala Gly Lys Lys Gly His Gly Ala Glu Leu Arg Leu Val

135

140

145

ccc cgc gcg tcc ccg ccc gca cgc ccc acc gtc gcg gga ttc gcg ggg 657

Pro Arg Ala Ser Pro Pro Ala Arg Pro Thr Val Ala Gly Phe Ala Gly

150

155

160

gag tcc aag ccc cgg gcc cgg aac cgg ggg cgg acc cgg gag cgt gcg 705

Glu Ser Lys Pro Arg Ala Arg Asn Arg Gly Arg Thr Arg Glu Arg Ala

165

170

175

180

tcc ggc cca gcc gct ggg acc ccg cct ccc caa agc gca ccg ccc aaa 753

Ser Gly Pro Ala Ala Gly Thr Pro Pro Pro Gln Ser Ala Pro Pro Lys

185

190

195

gaa aac ccc tca gag agg aag acc aac gtg ggc aag agg aag gcg gcc 801

Glu Asn Pro Ser Glu Arg Lys Thr Asn Val Gly Lys Arg Lys Ala Ala

200

205

210

ttg gtc ccc aac gag gag cga ccc atg ggg acc ggg ccc gac ccc gac 849

~~Leu Val Pro Asn Glu Glu Arg Pro Met Gly Thr Gly Pro Asp Pro Asp~~

215

220

225

ggg ctg gac ggg aac gcg gag ctc acg gag acc tac tgc gct gag aag 897

Gly Leu Asp Gly Asn Ala Glu Leu Thr Glu Thr Tyr Cys Ala Glu Lys

230

235

240

tgg cac tcc ctc tgc aac ttc ttt gtc aat ttc tgg aac ggc 939

Trp His Ser Leu Cys Asn Phe Phe Val Asn Phe Trp Asn Gly

245

250

255

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gggcgtctta gaccgggggg tactgtgata gagattgggg agaagtccag gttctcgaat 1059

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atctctggga tagcagagaa gttaaaaatt ttgaaaagtc tcagtcctga ttaagagcag 1179

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catgagcaat tgccaacctg agccagggtg aatcaatgtc ttctcactta atcagctaac 1419

aagactgcag acttttttct cgtttctgaa ttggtataaa cttggatgcg gcgtgggtggg 1479

~~tgatcatagat aacctctata gggacagaag cctcacaggt caagactggc tccaaggaaa 1539~~

gttttgcaga atgatttcct ttccattctt ttagaagagc tacctttttt ttttttttct 1599

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tatggctcac tgcggcctcg actttccagt ctcaagtgat cctctgcctc agcctccgga 1899

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atgttctgga actttcccat taaccttctg catttagaag gaattataga tgttgagtgc 2019

tccagtaaac agtgattctc tttatatctg atttttttt tttaaacagc taaaatgtaa 2079

gtatgtatct cagagtcatt ttgaccatta tggaagttaa atctctctgt ttcattgtaac 2139

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gtgctcaata aaaactgtat ggtagattt aaagaagtgg caaggcaatg gaaattctac 2259

ctgcatttga tctacttcca agtacacctt gaattaagtt cttaaacaca tcttgaattg 2319

ctgggaaaag acagaaacta agaagttgac ataaagcaag agtcacaaac tggcagccac 2379

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cccaccttcc tccatccat tgttgaatct gtggatgcag agccacgga tgtggagggg 2499

caactatata tatgttttcc cattatatat ataaatgtgt gtgtatgt 2547

<211> 258

<212> PRT

<213> Homo sapiens

<400> 102

Met Thr Pro Pro Lys Leu Arg Ala Ser Leu Ser Pro Ser Leu Leu Leu

1

5

10

15

Leu Leu Ser Gly Cys Leu Leu Ala Ala Ala Arg Arg Glu Lys Gly Ala

20

25

30

Ala Ser Asn Val Ala Glu Pro Val Pro Gly Pro Thr Gly Gly Ser Ser

35

40

45

Gly Arg Phe Leu Ser Pro Glu Gln His Ala Cys Ser Trp Gln Leu Leu

50

55

60

Leu Pro Ala Pro Glu Ala Ala Ala Gly Ser Glu Leu Ala Leu Arg Cys

65

70

75

80

~~Gln Ser Pro Asp Gly Ala Arg His Gln Cys Ala Tyr Arg Gly His Pro~~

85

90

95

Glu Arg Cys Ala Ala Tyr Ala Ala Arg Arg Ala His Phe Trp Lys Gln

100

105

110

Val Leu Gly Gly Leu Arg Lys Lys Arg Arg Pro Cys His Asp Pro Ala

115

120

125

Pro Leu Gln Ala Arg Leu Cys Ala Gly Lys Lys Gly His Gly Ala Glu
130 135 140

Leu Arg Leu Val Pro Arg Ala Ser Pro Pro Ala Arg Pro Thr Val Ala
145 150 155 160

Gly Phe Ala Gly Glu Ser Lys Pro Arg Ala Arg Asn Arg Gly Arg Thr
165 170 175

Arg Glu Arg Ala Ser Gly Pro Ala Ala Gly Thr Pro Pro Pro Gln Ser
180 185 190

Ala Pro Pro Lys Glu Asn Pro Ser Glu Arg Lys Thr Asn Val Gly Lys
195 200 205

Arg Lys Ala Ala Leu Val Pro Asn Glu Glu Arg Pro Met Gly Thr Gly
210 215 220

Pro Asp Pro Asp Gly Leu Asp Gly Asn Ala Glu Leu Thr Glu Thr Tyr
225 230 235 240

Cys Ala Glu Lys Trp His Ser Leu Cys Asn Phe Phe Val Asn Phe Trp
245 250 255

Asn Gly

<210> 103

<211> 1430

<212> DNA

<213> Homo. sapiens

<220>

<221> CDS

<222> (80)..(1333)

<400> 103

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ctactgtgac acacctacc atg cgg aca ctc ttc aac ctc ctc tgg ctt gcc 112

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala

1 5 10

ctg gcc tgc agc cct gtt cac act acc ctg tca aag tca gat gcc aaa 160

Leu Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys

15 20 25

aaa gcc gcc tca aag acg ctg ctg gag aag gtg aag ttt tgc tct tgt 208

Lys Ala Ala Ser Lys Thr Leu Leu Glu Lys Val Lys Phe Cys Ser Cys

30 35 40

tgc cca ggc tgg agc gca atg gcg cga tct tgg ctc acc gca acc tct 256

Cys Pro Gly Trp Ser Ala Met Ala Arg Ser Trp Leu Thr Ala Thr Ser

45 50 55

gcc acc cag agt cag ttt tca gat aag ccg gtg caa gac cgg ggt ttg 304

Ala Thr Gln Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg Gly Leu

60

65

70

75

gtg gtg acg gac ctc aaa gct gag agt gtg gtt ctt gag cat cgc agc 352

Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His Arg Ser

80

85

90

tac tgc tcg gca aag gcc cgg gac aga cac ttt gct ggg gat gta ctg 400

Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp Val Leu

95

100

105

ggc tat gtc act cca tgg aac agc cat ggc tac gat gtc acc aag gtc 448

Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val Thr Lys Val

110

115

120

ttt ggg agc aag ttc aca cag atc tca ccc gtc tgg ctg cag ctg aag 496

Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp Leu Gln Leu Lys

125

130

135

aga cgt ggc cgt gag atg ttt gag gtc acg ggc ctc cac gac gtg gac 544

Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu His Asp Val Asp

140

145

150

155

caa ggg tgg atg cga gct gtc agg aag cat gcc aag ggc ctg cac ata 592

Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys Gly Leu His Ile

160

165

170

gtg cct cgg ctc ctg ttt gag gac tgg act tac gat gat ttc cgg aac 640

Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp Phe Arg Asn

175

180

185

gtc tta gac agt gag gat gag ata gag gag ctg agc aag acc gtg gtc 688
 Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser Lys Thr Val Val
 190 195 200

cag gtg gca aag aac cag cat ttc gat ggc ttc gtg gtg gag gtc tgg 736
 Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val Val Glu Val Trp
 205 210 215

aac cag ctg cta agc cag aag cgc gtg ggc ctc atc cac atg ctc acc 784
 Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile His Met Leu Thr
 220 225 230 235

cac ttg gcc gag gct ctg cac cag gcc cgg ctg ctg gcc ctc ctg gtc 832
 His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu Ala Leu Leu Val
 240 245 250

atc ccg cct gcc atc acc ccc ggg acc gac cag ctg ggc atg ttc acg 880
 Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu Gly Met Phe Thr
 255 260 265

cac aag gag ttt gag cag ctg gcc ccc gtg ctg gat ggt ttc agc ctc 928
 His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp Gly Phe Ser Leu
 270 275 280

atg acc tac gac tac tct aca gcg cat cag cct ggc cct aat gca ccc 976
 Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly Pro Asn Ala Pro
 285 290 295

ctg tcc tgg gtt cga gcc tgc gtc cag gtc ctg gac ccg aag tcc aag 1024
 Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp Pro Lys Ser Lys
 300 305 310 315

tgg cga agc aaa atc ctc ctg ggg ctc aac ttc tat ggt atg gac tac 1072
 Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr Gly Met Asp Tyr
 320 325 330

gcg acc tcc aag gat gcc cgt gag cct gtt gtc ggg gcc agg tac atc 1120
 Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly Ala Arg Tyr Ile
 335 340 345

cag aca ctg aag gac cac agg ccc cgg atg gtg tgg gac agc cag gcc 1168
 Gln Thr Leu Lys Asp His Arg Pro Arg Met Val Trp Asp Ser Gln Ala
 350 355 360

tca gag cac ttc ttc gag tac aag aag agc cgc agt ggg agg cac gtc 1216
 Ser Glu His Phe Phe Glu Tyr Lys Lys Ser Arg Ser Gly Arg His Val
 365 370 375

gtc ttc tac cca acc ctg aag tcc ctg cag gtg cgg ctg gag ctg gcc 1264
 Val Phe Tyr Pro Thr Leu Lys Ser Leu Gln Val Arg Leu Glu Leu Ala
 380 385 390 395

cgg gag ctg ggc gtt ggg gtc tct atc tgg gag ctg ggc cag ggc ctg 1312
 Arg Glu Leu Gly Val Gly Val Ser Ile Trp Glu Leu Gly Gln Gly Leu
 400 405 410

gac tac ttc tac gac ctg ctc taggtgggca ttgcggcctc cgcggtggac 1363

Asp Tyr Phe Tyr Asp Leu Leu

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gtgttctttt ctaagccatg gagtgagtga gcaggtgtga aatacaggcc tccctccgtt 1423

tgctgtg

1430

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<212> PRT

<213> Homo sapiens

<400> 104

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro

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Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys

20

25

30

Thr Leu Leu Glu Lys Val Lys Phe Cys Ser Cys Cys Pro Gly Trp Ser

35

40

45

Ala Met Ala Arg Ser Trp Leu Thr Ala Thr Ser Ala Thr Gln Ser Gln

50

55

60

Phe Ser Asp Lys Pro Val Gln Asp Arg Gly Leu Val Val Thr Asp Leu

65

70

75

80

Lys Ala Glu Ser Val Val Leu Glu His Arg Ser Tyr Cys Ser Ala Lys

85

90

95

Ala Arg Asp Arg His Phe Ala Gly Asp Val Leu Gly Tyr Val Thr Pro

100

105

110

Trp Asn Ser His Gly Tyr Asp Val Thr Lys Val Phe Gly Ser Lys Phe

115

120

125

Thr Gln Ile Ser Pro Val Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu

130

135

140

Met Phe Glu Val Thr Gly Leu His Asp Val Asp Gln Gly Trp Met Arg

145

150

155

160

Ala Val Arg Lys His Ala Lys Gly Leu His Ile Val Pro Arg Leu Leu

165

170

175

Phe Glu Asp Trp Thr Tyr Asp Asp Phe Arg Asn Val Leu Asp Ser Glu

180

185

190

Asp Glu Ile Glu Glu Leu Ser Lys Thr Val Val Gln Val Ala Lys Asn

195

200

205

Gln His Phe Asp Gly Phe Val Val Glu Val Trp Asn Gln Leu Leu Ser

210

215

220

Gln Lys Arg Val Gly Leu Ile His Met Leu Thr His Leu Ala Glu Ala

225

230

235

240

Leu His Gln Ala Arg Leu Leu Ala Leu Leu Val Ile Pro Pro Ala Ile
245 250 255

Thr Pro Gly Thr Asp Gln Leu Gly Met Phe Thr His Lys Glu Phe Glu
260 265 270

Gln Leu Ala Pro Val Leu Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr
275 280 285

Ser Thr Ala His Gln Pro Gly Pro Asn Ala Pro Leu Ser Trp Val Arg
290 295 300

Ala Cys Val Gln Val Leu Asp Pro Lys Ser Lys Trp Arg Ser Lys Ile
305 310 315 320

Leu Leu Gly Leu Asn Phe Tyr Gly Met Asp Tyr Ala Thr Ser Lys Asp
325 330 335

Ala Arg Glu Pro Val Val Gly Ala Arg Tyr Ile Gln Thr Leu Lys Asp
340 345 350

His Arg Pro Arg Met Val Trp Asp Ser Gln Ala Ser Glu His Phe Phe
355 360 365

Glu Tyr Lys Lys Ser Arg Ser Gly Arg His Val Val Phe Tyr Pro Thr
370 375 380

Leu Lys Ser Leu Gln Val Arg Leu Glu Leu Ala Arg Glu Leu Gly Val

○

385

390

395

400

Gly Val Ser Ile Trp Glu Leu Gly Gln Gly Leu Asp Tyr Phe Tyr Asp

405

410

415

Leu Leu

<210> 105

<211> 2506

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (24)..(1505)

<400> 105

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Met Ala Arg Ala Pro Pro Leu Leu Ala Ala

1

5

10

ttg acc gcg ctc ctc gcc gcc gcc gct gct ggc gga gat gcc ccg ccg 101

Leu Thr Ala Leu Leu Ala Ala Ala Ala Ala Gly Gly Asp Ala Pro Pro

15

20

25

ggc aaa atc gcg gtg gtt ggg gct ggg att ggg ggc tct gct gtg gcc 149

Gly Lys Ile Ala Val Val Gly Ala Gly Ile Gly Gly Ser Ala Val Ala

30

35

40

cat ttt ctc cag cag cac ttc gga cct cgg gtg cag atc gac gtg tac 197

His Phe Leu Gln Gln His Phe Gly Pro Arg Val Gln Ile Asp Val Tyr

45

50

55

gag aag gga acc gtg ggt ggc cgc ttg gcc acc atc tca gtc aac aag 245

Glu Lys Gly Thr Val Gly Gly Arg Leu Ala Thr Ile Ser Val Asn Lys

60

65

70

cag cac tat gag agc ggg gct gcc tcc ttc cac tcc ctg agc ctg cac 293

Gln His Tyr Glu Ser Gly Ala Ala Ser Phe His Ser Leu Ser Leu His

75

80

85

90

atg cag gac ttc gtc aag ctg ctg ggg ctg agg cac cgg cgc gag gtg 341

Met Gln Asp Phe Val Lys Leu Leu Gly Leu Arg His Arg Arg Glu Val

95

100

105

gtg ggc agg agc gcc atc ttc ggc ggg gag cac ttc atg ctg gag gag 389

Val Gly Arg Ser Ala Ile Phe Gly Gly Glu His Phe Met Leu Glu Glu

110

115

120

act gac tgg tac ctg ctg aac ctc ttc cgc ctc tgg tgg cac tat ggc 437

Thr Asp Trp Tyr Leu Leu Asn Leu Phe Arg Leu Trp Trp His Tyr Gly

125

130

135

atc agc ttc ctg agg ctg cag atg tgg gtg gag gag gtc atg gag aag 485

Ile Ser Phe Leu Arg Leu Gln Met Trp Val Glu Glu Val Met Glu Lys

140

145

150

ttc atg agg atc tat aag tac cag gcc cac ggc tat gcc ttc tcg ggt 533

Phe Met Arg Ile Tyr Lys Tyr Gln Ala His Gly Tyr Ala Phe Ser Gly

155 160 165 170

gtg gag gag ctg ctc tac tca ctg ggg gag tcc acc ttt gtt aac atg 581

Val Glu Glu Leu Leu Tyr Ser Leu Gly Glu Ser Thr Phe Val Asn Met

175 180 185

acc cag cac tct gtg gct gag tcc ctg ctg cag gtg ggc gtc acg cag 629

Thr Gln His Ser Val Ala Glu Ser Leu Leu Gln Val Gly Val Thr Gln

190 195 200

cgc ttt att gat gat gtc gtt tct gct gtc ctg cgg gcc agc tat ggc 677

Arg Phe Ile Asp Asp Val Val Ser Ala Val Leu Arg Ala Ser Tyr Gly

205 210 215

cag tca gca gcg atg ccc gcc ttt gca gga gcc atg tca cta gcc ggg 725

Gln Ser Ala Ala Met Pro Ala Phe Ala Gly Ala Met Ser Leu Ala Gly

220 225 230

gcc caa ggc agc ctg tgg tct gtg gaa gga ggc aat aag ctg gtt tgt 773

Ala Gln Gly Ser Leu Trp Ser Val Glu Gly Gly Asn Lys Leu Val Cys

235 240 245 250

tcc ggt ttg ctg aag ctc acc aag gcc aat gtg atc cat gcc aca gtg 821

Ser Gly Leu Leu Lys Leu Thr Lys Ala Asn Val Ile His Ala Thr Val

255 260 265

acc tct gtg acc ctg cac agc aca gag ggg aaa gcc ctg tac cag gtg 869
 Thr Ser Val Thr Leu His Ser Thr Glu Gly Lys Ala Leu Tyr Gln Val
 270 275 280

gcg tat gag aat gag gta ggc aac agc tct gac ttc tat gac atc gtg 917
 Ala Tyr Glu Asn Glu Val Gly Asn Ser Ser Asp Phe Tyr Asp Ile Val
 285 290 295

gtc atc gcc acc ccc ctg cac ctg gac aac agc agc agc aac tta acc 965
 Val Ile Ala Thr Pro Leu His Leu Asp Asn Ser Ser Ser Asn Leu Thr
 300 305 310

ttt gca ggc ttc cac ccg ccc att gat gac gtg cag ggc tct ttc cag 1013
 Phe Ala Gly Phe His Pro Pro Ile Asp Asp Val Gln Gly Ser Phe Gln
 315 320 325 330

ccc acc gtc gtc tcc ttg gtc cac ggc tac ctc aac tcg tcc tac ttc 1061
 Pro Thr Val Val Ser Leu Val His Gly Tyr Leu Asn Ser Ser Tyr Phe
 335 340 345

ggt ttc cca gac cct aag ctt ttc ccc ttt gcc aac atc ctt acc aca 1109
 Gly Phe Pro Asp Pro Lys Leu Phe Pro Phe Ala Asn Ile Leu Thr Thr
 350 355 360

gat ttc ccc agc ttc ttc tgc act ctg gac aac atc tgc cct gtc aac 1157
 Asp Phe Pro Ser Phe Phe Cys Thr Leu Asp Asn Ile Cys Pro Val Asn
 365 370 375

atc tct gcc agc ttc cgg cga aag cag ccc cag gag gca gct gtt tgg 1205

Ile Ser Ala Ser Phe Arg Arg Lys Gln Pro Gln Glu Ala Ala Val Trp
380 385 390

cga gtc cag tcc ccc aag ccc ctc ttt cgg acc cag cta aag acc ctg 1253
Arg Val Gln Ser Pro Lys Pro Leu Phe Arg Thr Gln Leu Lys Thr Leu
395 400 405 410

ttc cgt tcc tat tac tca gtg cag aca gct gag tgg cag gcc cat ccc 1301
Phe Arg Ser Tyr Tyr Ser Val Gln Thr Ala Glu Trp Gln Ala His Pro
415 420 425

ctc tat ggc tcc cgc ccc acg ctc ccg agg ttt gca ctc cat gac cag 1349
Leu Tyr Gly Ser Arg Pro Thr Leu Pro Arg Phe Ala Leu His Asp Gln
430 435 440

ctc ttc tac ctc aat gcc ctg gag tgg gcg gcc agc tcc gtg gag gtg 1397
Leu Phe Tyr Leu Asn Ala Leu Glu Trp Ala Ala Ser Ser Val Glu Val
445 450 455

atg gcc gtg gct gcc aag aat gtg gcc ttg ctg gct tac aac cgc tgg 1445
Met Ala Val Ala Ala Lys Asn Val Ala Leu Leu Ala Tyr Asn Arg Trp
460 465 470

tac cag gac cta gac aag att gat caa aaa gat ttg atg cac aag gtc 1493
Tyr Gln Asp Leu Asp Lys Ile Asp Gln Lys Asp Leu Met His Lys Val
475 480 485 490

aag act gaa ctg tgagggtctt agggagagcc tgggaacttt catccccac 1545
Lys Thr Glu Leu

tgaagatgga tcatcccaca gcagcccagg actgaataag ccatgctcgc ccaccaggct 1605

tctttctgac ccctcatgta tcaagcatct ccaggtgacc tactgtctgc ctatattaag 1665

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gtgcttcaga cttggtttct tagctagaaa ccagaagact acgggaggga atataaggca 1845

gagaactatg agtcttattt tattactgtt tttcactacc tactcccaca atggacaatc 1905

aattgaggca acctacaaga aaacatttac aaccagatgg ttacaaataa agtagaaggg 1965

aagatcagaa aacctagaa atgatcatag ctccctggta ctgtggactt gatagatttg 2025

aggtacctag ttcagaactc cctagtcacc atctccaagc ctgtcaacat cactgcatat 2085

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cctgggtactt tctcatcgga cactagcttg aagtaagagg agaattatgc ttttctttgc 2445

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2506

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<211> 494

<212> PRT

<213> Homo sapiens

<400> 106

Met Ala Arg Ala Pro Pro Leu Leu Ala Ala Leu Thr Ala Leu Leu Ala

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Ala Ala Ala Ala Gly Gly Asp Ala Pro Pro Gly Lys Ile Ala Val Val

20 25 30

Gly Ala Gly Ile Gly Gly Ser Ala Val Ala His Phe Leu Gln Gln His

35 40 45

Phe Gly Pro Arg Val Gln Ile Asp Val Tyr Glu Lys Gly Thr Val Gly

50 55 60

Gly Arg Leu Ala Thr Ile Ser Val Asn Lys Gln His Tyr Glu Ser Gly

65 70 75 80

Ala Ala Ser Phe His Ser Leu Ser Leu His Met Gln Asp Phe Val Lys

85

90

95

Leu Leu Gly Leu Arg His Arg Arg Glu Val Val Gly Arg Ser Ala Ile

100

105

110

Phe Gly Gly Glu His Phe Met Leu Glu Glu Thr Asp Trp Tyr Leu Leu

115

120

125

Asn Leu Phe Arg Leu Trp Trp His Tyr Gly Ile Ser Phe Leu Arg Leu

130

135

140

Gln Met Trp Val Glu Glu Val Met Glu Lys Phe Met Arg Ile Tyr Lys

145

150

155

160

Tyr Gln Ala His Gly Tyr Ala Phe Ser Gly Val Glu Glu Leu Leu Tyr

165

170

175

Ser Leu Gly Glu Ser Thr Phe Val Asn Met Thr Gln His Ser Val Ala

180

185

190

Glu Ser Leu Leu Gln Val Gly Val Thr Gln Arg Phe Ile Asp Asp Val

195

200

205

Val Ser Ala Val Leu Arg Ala Ser Tyr Gly Gln Ser Ala Ala Met Pro

210

215

220

Ala Phe Ala Gly Ala Met Ser Leu Ala Gly Ala Gln Gly Ser Leu Trp

225

230

235

240

Ser Val Glu Gly Gly Asn Lys Leu Val Cys Ser Gly Leu Leu Lys Leu
245 250 255

Thr Lys Ala Asn Val Ile His Ala Thr Val Thr Ser Val Thr Leu His
260 265 270

Ser Thr Glu Gly Lys Ala Leu Tyr Gln Val Ala Tyr Glu Asn Glu Val
275 280 285

Gly Asn Ser Ser Asp Phe Tyr Asp Ile Val Val Ile Ala Thr Pro Leu
290 295 300

His Leu Asp Asn Ser Ser Ser Asn Leu Thr Phe Ala Gly Phe His Pro
305 310 315 320

Pro Ile Asp Asp Val Gln Gly Ser Phe Gln Pro Thr Val Val Ser Leu
325 330 335

Val His Gly Tyr Leu Asn Ser Ser Tyr Phe Gly Phe Pro Asp Pro Lys
340 345 350

Leu Phe Pro Phe Ala Asn Ile Leu Thr Thr Asp Phe Pro Ser Phe Phe
355 360 365

Cys Thr Leu Asp Asn Ile Cys Pro Val Asn Ile Ser Ala Ser Phe Arg
370 375 380

Arg Lys Gln Pro Gln Glu Ala Ala Val Trp Arg Val Gln Ser Pro Lys
385 390 395 400

Pro Leu Phe Arg Thr Gln Leu Lys Thr Leu Phe Arg Ser Tyr Tyr Ser

405

410

415

Val Gln Thr Ala Glu Trp Gln Ala His Pro Leu Tyr Gly Ser Arg Pro

420

425

430

Thr Leu Pro Arg Phe Ala Leu His Asp Gln Leu Phe Tyr Leu Asn Ala

435

440

445

Leu Glu Trp Ala Ala Ser Ser Val Glu Val Met Ala Val Ala Ala Lys

450

455

460

Asn Val Ala Leu Leu Ala Tyr Asn Arg Trp Tyr Gln Asp Leu Asp Lys

465

470

475

480

Ile Asp Gln Lys Asp Leu Met His Lys Val Lys Thr Glu Leu

485

490

<210> 107

<211> 2465

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (457)..(1434)

<400> 107

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ctggtgcagc ttagcaagag ggcccaggat ttttgatcc ccagccctgt gacaagggtt 180

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gcctcgtctc cctgactgtc cgcaggcctg ggcagc atg gcc gta ttc cgg tcg 474

Met Ala Val Phe Arg Ser

1

5

ggt ctc ctg gtg ctg acg acg ccg ctg gcc tcc cta gcc cct cgc ctg 522

Gly Leu Leu Val Leu Thr Thr Pro Leu Ala Ser Leu Ala Pro Arg Leu

10

15

20

gcc tcc atc ctg acc tcg gcg gcc cgg ctg gtg aat cac aca ctc tat 570

Ala Ser Ile Leu Thr Ser Ala Ala Arg Leu Val Asn His Thr Leu Tyr

25

30

35

gtt cac ctg cag ccg ggc atg agc ctg gag ggc ccg gct cag ccc cag 618

Val His Leu Gln Pro Gly Met Ser Leu Glu Gly Pro Ala Gln Pro Gln

40

45

50

tac agc ccc gtg cag gcc acg ttt gag gtt ctt gat ttc atc acg cac 666
Tyr Ser Pro Val Gln Ala Thr Phe Glu Val Leu Asp Phe Ile Thr His
55 60 65 70

ctc tat gct ggc gcc gac gtc cac agg cac ttg gac gtc aga atc cta 714
Leu Tyr Ala Gly Ala Asp Val His Arg His Leu Asp Val Arg Ile Leu
75 80 85

ctg acc aat atc cga acc aag agc acc ttt ctc cct ccc ctg ccc acc 762
Leu Thr Asn Ile Arg Thr Lys Ser Thr Phe Leu Pro Pro Leu Pro Thr
90 95 100

tca gtc cag aat ctc gcc cac ccg cca gaa gtc gtg ttg aca gat ttc 810
Ser Val Gln Asn Leu Ala His Pro Pro Glu Val Val Leu Thr Asp Phe
105 110 115

cag acc ctg gat gga agc cag tac aac ccg gtc aaa cag cag cta gtg 858
Gln Thr Leu Asp Gly Ser Gln Tyr Asn Pro Val Lys Gln Gln Leu Val
120 125 130

cgt tac gcc acc agc tgt tac agc tgt tgt ccg cga ctg gcc tcg gtg 906
Arg Tyr Ala Thr Ser Cys Tyr Ser Cys Cys Pro Arg Leu Ala Ser Val
135 140 145 150

ctg cta tac tcc gat tat ggg ata gga gaa gtg ccc gtg gag ccc ctg 954
Leu Leu Tyr Ser Asp Tyr Gly Ile Gly Glu Val Pro Val Glu Pro Leu
155 160 165

gat gtc ccc tta ccc tcc acg atc agg cca gct tcc ccc gtg gcc ggg 1002

Asp Val Pro Leu Pro Ser Thr Ile Arg Pro Ala Ser Pro Val Ala Gly

170

175

180

tct cca aag cag ccg gtg cgt ggc tac tac cgt ggc gct gtc ggt ggc 1050

Ser Pro Lys Gln Pro Val Arg Gly Tyr Tyr Arg Gly Ala Val Gly Gly

185

190

195

acg ttt gac cgc ctg cac aac gcc cac aag gtg ttg ctc agt gtc gcg 1098

Thr Phe Asp Arg Leu His Asn Ala His Lys Val Leu Leu Ser Val Ala

200

205

210

tgc atc ctg gcc cag gag cag ctt gtg gtg gga gta gca gac aaa gat 1146

Cys Ile Leu Ala Gln Glu Gln Leu Val Val Gly Val Ala Asp Lys Asp

215

220

225

230

ctg ttg aag agc aag ttg ctc cct gag ctg ctc caa cct tat aca gaa 1194

Leu Leu Lys Ser Lys Leu Leu Pro Glu Leu Leu Gln Pro Tyr Thr Glu

235

240

245

cgt gtg gaa cat ctg agt gaa ttc ctg gtg gac atc aag ccc tcc ttg 1242

Arg Val Glu His Leu Ser Glu Phe Leu Val Asp Ile Lys Pro Ser Leu

250

255

260

act ttt gat gtc atc ccc ctg ctg gac ccc tat ggg ccc gct ggc tct 1290

Thr Phe Asp Val Ile Pro Leu Leu Asp Pro Tyr Gly Pro Ala Gly Ser

265

270

275

gac ccc tcc ctg gag ttc ctg gtg gtc agc gag gag acc tat cgt ggg 1338

Asp Pro Ser Leu Glu Phe Leu Val Val Ser Glu Glu Thr Tyr Arg Gly

280

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290

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Gly Met Ala Ile Asn Arg Phe Arg Leu Glu Asn Asp Leu Glu Glu Leu

295

300

305

310

gct ttg tac caa gat cca gct gct gaa gga cct cag aca tac gga gaa 1434

Ala Leu Tyr Gln Asp Pro Ala Ala Glu Gly Pro Gln Thr Tyr Gly Glu

315

320

325

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30

Val Asn His Thr Leu Tyr Val His Leu Gln Pro Gly Met Ser Leu Glu

35

40

45

Gly Pro Ala Gln Pro Gln Tyr Ser Pro Val Gln Ala Thr Phe Glu Val

50

55

60

Leu Asp Phe Ile Thr His Leu Tyr Ala Gly Ala Asp Val His Arg His

65

70

75

80

Leu Asp Val Arg Ile Leu Leu Thr Asn Ile Arg Thr Lys Ser Thr Phe

85

90

95

Leu Pro Pro Leu Pro Thr Ser Val Gln Asn Leu Ala His Pro Pro Glu

100

105

110

Val Val Leu Thr Asp Phe Gln Thr Leu Asp Gly Ser Gln Tyr Asn Pro

115

120

125

Val Lys Gln Gln Leu Val Arg Tyr Ala Thr Ser Cys Tyr Ser Cys Cys

130

135

140

Pro Arg Leu Ala Ser Val Leu Leu Tyr Ser Asp Tyr Gly Ile Gly Glu

145

150

155

160

Val Pro Val Glu Pro Leu Asp Val Pro Leu Pro Ser Thr Ile Arg Pro

165

170

175

Ala Ser Pro Val Ala Gly Ser Pro Lys Gln Pro Val Arg Gly Tyr Tyr

180

185

190

Arg Gly Ala Val Gly Gly Thr Phe Asp Arg Leu His Asn Ala His Lys

195

200

205

Val Leu Leu Ser Val Ala Cys Ile Leu Ala Gln Glu Gln Leu Val Val

210

215

220

Gly Val Ala Asp Lys Asp Leu Leu Lys Ser Lys Leu Leu Pro Glu Leu

225

230

235

240

Leu Gln Pro Tyr Thr Glu Arg Val Glu His Leu Ser Glu Phe Leu Val

245

250

255

Asp Ile Lys Pro Ser Leu Thr Phe Asp Val Ile Pro Leu Leu Asp Pro

260

265

270

Tyr Gly Pro Ala Gly Ser Asp Pro Ser Leu Glu Phe Leu Val Val Ser

275

280

285

Glu Glu Thr Tyr Arg Gly Gly Met Ala Ile Asn Arg Phe Arg Leu Glu

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Asn Asp Leu Glu Glu Leu Ala Leu Tyr Gln Asp Pro Ala Ala Glu Gly

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Pro Gln Thr Tyr Gly Glu

325

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Met Ser Ser Ser Gly

1 5

ggg gcg ccc ggg gcg tcc gcc agc tct gcg ccg ccc gcg cag gaa gag 163

Gly Ala Pro Gly Ala Ser Ala Ser Ser Ala Pro Pro Ala Gln Glu Glu

10 15 20

ggc atg acg tgg tgg tac cgc tgg ctg tgt cgc ctg tct ggg gtg ctg 211

Gly Met Thr Trp Trp Tyr Arg Trp Leu Cys Arg Leu Ser Gly Val Leu

25 30 35

ggg gca gtc tct tgc gcg atc tct ggc ctc ttc aac tgc atc acc atc 259

Gly Ala Val Ser Cys Ala Ile Ser Gly Leu Phe Asn Cys Ile Thr Ile

40	45	50	
cac cct ctg aac atc gcg gcc ggc gtg tgg atg atg atg gcg gtc gtt			307
His Pro Leu Asn Ile Ala Ala Gly Val Trp Met Met Met Ala Val Val			
55	60	65	

ccc atc gtc atc agc ctg acc ctg acc acg ctg ctg ggc aac gcc atc			355
Pro Ile Val Ile Ser Leu Thr Leu Thr Thr Leu Leu Gly Asn Ala Ile			
70	75	80	85

gcc ttt gct acg ggg gtg ctg tac gga ctc tct gct ctg ggc aaa aag			403
Ala Phe Ala Thr Gly Val Leu Tyr Gly Leu Ser Ala Leu Gly Lys Lys			
90	95	100	

ggc gat gcg atc tcc tat gcc agg atc cag cag cag agg cag cag gcg			451
Gly Asp Ala Ile Ser Tyr Ala Arg Ile Gln Gln Gln Arg Gln Gln Ala			
105	110	115	

gat gag gag aag ctc gcg gag acc ctg gag ggg gag ctg tgaagggctg			500
Asp Glu Glu Lys Leu Ala Glu Thr Leu Glu Gly Glu Leu			
120	125	130	

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2557

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<212> PRT

<213> Homo sapiens

<400> 110

Met Ser Ser Ser Gly Gly Ala Pro Gly Ala Ser Ala Ser Ser Ala Pro

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Pro Ala Gln Glu Glu Gly Met Thr Trp Trp Tyr Arg Trp Leu Cys Arg

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Leu Ser Gly Val Leu Gly Ala Val Ser Cys Ala Ile Ser Gly Leu Phe

35

40

45

Asn Cys Ile Thr Ile His Pro Leu Asn Ile Ala Ala Gly Val Trp Met

50

55

60

Met Met Ala Val Val Pro Ile Val Ile Ser Leu Thr Leu Thr Thr Leu

65

70

75

80

Leu Gly Asn Ala Ile Ala Phe Ala Thr Gly Val Leu Tyr Gly Leu Ser

85

90

95

Ala Leu Gly Lys Lys Gly Asp Ala Ile Ser Tyr Ala Arg Ile Gln Gln

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Gln Arg Gln Gln Ala Asp Glu Glu Lys Leu Ala Glu Thr Leu Glu Gly

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Glu Leu

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<400> 111

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gtcatctata atttcctgag cctgtgctat gagtacctag gaggagaaag ttccatc 117

atg tcg gag atc aga gga aaa ccc att gag tcc agc tgt atg tat ggc 165

Met Ser Glu Ile Arg Gly Lys Pro Ile Glu Ser Ser Cys Met Tyr Gly

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acc tgc tgc ctc tgg gga aag act tat tcc atc gga ttt ctg agg ttc 213

Thr Cys Cys Leu Trp Gly Lys Thr Tyr Ser Ile Gly Phe Leu Arg Phe

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25

30

tgc aaa cag gcc acc ctg cag ttc tgt gtg gtg aag cca ctc atg gcg 261

Cys Lys Gln Ala Thr Leu Gln Phe Cys Val Val Lys Pro Leu Met Ala

35

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gtc agc act gtg gtc ctc cag gcc ttc ggc aag tac cgg gat ggg gac 309

Val Ser Thr Val Val Leu Gln Ala Phe Gly Lys Tyr Arg Asp Gly Asp

50

55

60

ttt gac gtc acc agt ggc tac ctc tac gtg acc atc atc tgc aac atc 357

Phe Asp Val Thr Ser Gly Tyr Leu Tyr Val Thr Ile Ile Cys Asn Ile

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70

75

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tcc gtc agc ctg gcc ctc tac gcc ctc ttc ctc ttc tac ttc gcc acc 405

Ser Val Ser Leu Ala Leu Tyr Ala Leu Phe Leu Phe Tyr Phe Ala Thr

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90

95

cgg gag ctg ctc agc ccc tac agc ccc gtc ctc aag ttc ttc atg gtc 453

Arg Glu Leu Leu Ser Pro Tyr Ser Pro Val Leu Lys Phe Phe Met Val

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105

110

aag tcc gtc atc ttt ctt tcc ttc tgg caa ggc atg ctc ctg gcc atc 501

Lys Ser Val Ile Phe Leu Ser Phe Trp Gln Gly Met Leu Leu Ala Ile

115

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ctg gag aag tgt ggg gcc atc ccc aaa atc cac tcg gcc cgc gtg tcg 549

Leu Glu Lys Cys Gly Ala Ile Pro Lys Ile His Ser Ala Arg Val Ser
130 135 140

gtg ggc gag ggc acc gtg gct gcc ggc tac cag gac ttc atc atc tgt 597
Val Gly Glu Gly Thr Val Ala Ala Gly Tyr Gln Asp Phe Ile Ile Cys
145 150 155 160

gtg gag atg ttc ttt gca gcc ctg gcc ctg cgg cac gcc ttc acc tac 645
Val Glu Met Phe Phe Ala Ala Leu Ala Leu Arg His Ala Phe Thr Tyr
165 170 175

aag gtc tat gct gac aag agg ctg gac gca caa ggc cgc tgt gcc ccc 693
Lys Val Tyr Ala Asp Lys Arg Leu Asp Ala Gln Gly Arg Cys Ala Pro
180 185 190

atg aag agc atc tcc agc agc ctc aag gag acc atg aac ccg cac gac 741
Met Lys Ser Ile Ser Ser Ser Leu Lys Glu Thr Met Asn Pro His Asp
195 200 205

atc gtg cag gac gcc atc cac aac ttc tca cct gcc tac cag cag tac 789
Ile Val Gln Asp Ala Ile His Asn Phe Ser Pro Ala Tyr Gln Gln Tyr
210 215 220

acg ctg cag tcc acc ctg gag cct ggg ccc acc tgg cgt ggt ggc gcc 837
Thr Leu Gln Ser Thr Leu Glu Pro Gly Pro Thr Trp Arg Gly Gly Ala
225 230 235 240

cac ggc ctc tcc cgc tcc cac agc ctc agt ggc gcc cgc gac aac gag 885
His Gly Leu Ser Arg Ser His Ser Leu Ser Gly Ala Arg Asp Asn Glu

245

250

255

aag act ctc ctg ctc agc tct gat gat gaa ttc taggtgcggg ctgcagtggc 938

Lys Thr Leu Leu Leu Ser Ser Asp Asp Glu Phe

260

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<400> 112

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20 25 30

Cys Lys Gln Ala Thr Leu Gln Phe Cys Val Val Lys Pro Leu Met Ala
35 40 45

Val Ser Thr Val Val Leu Gln Ala Phe Gly Lys Tyr Arg Asp Gly Asp
50 55 60

Phe Asp Val Thr Ser Gly Tyr Leu Tyr Val Thr Ile Ile Cys Asn Ile
65 70 75 80

Ser Val Ser Leu Ala Leu Tyr Ala Leu Phe Leu Phe Tyr Phe Ala Thr
85 90 95

Arg Glu Leu Leu Ser Pro Tyr Ser Pro Val Leu Lys Phe Phe Met Val
100 105 110

Lys Ser Val Ile Phe Leu Ser Phe Trp Gln Gly Met Leu Leu Ala Ile
115 120 125

Leu Glu Lys Cys Gly Ala Ile Pro Lys Ile His Ser Ala Arg Val Ser
130 135 140

Val Gly Glu Gly Thr Val Ala Ala Gly Tyr Gln Asp Phe Ile Ile Cys
145 150 155 160

Val Glu Met Phe Phe Ala Ala Leu Ala Leu Arg His Ala Phe Thr Tyr
 165 170 175

Lys Val Tyr Ala Asp Lys Arg Leu Asp Ala Gln Gly Arg Cys Ala Pro
 180 185 190

Met Lys Ser Ile Ser Ser Ser Leu Lys Glu Thr Met Asn Pro His Asp
 195 200 205

Ile Val Gln Asp Ala Ile His Asn Phe Ser Pro Ala Tyr Gln Gln Tyr
 210 215 220

Thr Leu Gln Ser Thr Leu Glu Pro Gly Pro Thr Trp Arg Gly Gly Ala
 225 230 235 240

His Gly Leu Ser Arg Ser His Ser Leu Ser Gly Ala Arg Asp Asn Glu
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Lys Thr Leu Leu Leu Ser Ser Asp Asp Glu Phe
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<210> 113

<211> 2563

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<222> (31)..(2238)

<400> 113

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Leu Thr Thr Leu Leu Ala Val Val Ala Ala Ala Ser Gln Ala Glu Val

10

15

20

gag tcc gag gca gga tgg ggc atg gtg acg cct gat ctg ctc ttc gcc 150

Glu Ser Glu Ala Gly Trp Gly Met Val Thr Pro Asp Leu Leu Phe Ala

25

30

35

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gag ggg acc gca gcc tac gcg cgc ggg gac tgg ccc ggg gtg gtc ctg 198

Glu Gly Thr Ala Ala Tyr Ala Arg Gly Asp Trp Pro Gly Val Val Leu

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agc atg gaa cgg gcg ctg cgc tcc cgg gca gcc ctc cgc gcc ctt cgc 246

Ser Met Glu Arg Ala Leu Arg Ser Arg Ala Ala Leu Arg Ala Leu Arg

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Leu Arg Cys Arg Thr Gln Cys Ala Ala Asp Phe Pro Trp Glu Leu Asp

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ccc gac tgg tcc ccc agc ccg gcc cag gcc tcg ggc gcc gcc gcc ctg 342

Pro Asp Trp Ser Pro Ser Pro Ala Gln Ala Ser Gly Ala Ala Ala Leu
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 Arg Asp Leu Ser Phe Phe Gly Gly Leu Leu Arg Arg Ala Ala Cys Leu
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cgc cgc tgc ctc ggg ccg ccg gcc gcc cac tcg ctc agc gaa gag atg 438
 Arg Arg Cys Leu Gly Pro Pro Ala Ala His Ser Leu Ser Glu Glu Met
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gag ctg gag ttc cgc aag cgg agc ccc tac aac tac ctg cag gtc gcc 486
 Glu Leu Glu Phe Arg Lys Arg Ser Pro Tyr Asn Tyr Leu Gln Val Ala
 140 145 150

tac ttc aag atc aac aag ttg gag aaa gct gtt gct gca gca cac acc 534
 Tyr Phe Lys Ile Asn Lys Leu Glu Lys Ala Val Ala Ala Ala His Thr
 155 160 165

ttc ttc gtg ggc aat cct gag cac atg gaa atg cag cag aac cta gac 582
 Phe Phe Val Gly Asn Pro Glu His Met Glu Met Gln Gln Asn Leu Asp
 170 175 180

tat tac caa acc atg tct gga gtg aag gag gcc gac ttc aag gat ctt 630
 Tyr Tyr Gln Thr Met Ser Gly Val Lys Glu Ala Asp Phe Lys Asp Leu
 185 190 195 200

gag act caa ccc cat atg caa gaa ttt cga ctg gga gtg cga ctc tac 678
 Glu Thr Gln Pro His Met Gln Glu Phe Arg Leu Gly Val Arg Leu Tyr

205	210	215	
tca gag gaa cag cca cag gaa gct gtg ccc cac cta gag gcg gcg ctg			726
Ser Glu Glu Gln Pro Gln Glu Ala Val Pro His Leu Glu Ala Ala Leu			
220	225	230	

235	240	245	
caa gaa tac ttt gtg gcc tat gag gag tgc cgt gcc ctc tgc gaa ggg			774
Gln Glu Tyr Phe Val Ala Tyr Glu Glu Cys Arg Ala Leu Cys Glu Gly			

250	255	260	
ccc tat gac tac gat ggc tac aac tac ctt gag tac aac gct gac ctc			822
Pro Tyr Asp Tyr Asp Gly Tyr Asn Tyr Leu Glu Tyr Asn Ala Asp Leu			

265	270	275	280	
ttc cag gcc atc aca gat cat tac atc cag gtc ctc aac tgt aag cag				870
Phe Gln Ala Ile Thr Asp His Tyr Ile Gln Val Leu Asn Cys Lys Gln				

285	290	295	
aac tgt gtc acg gag ctt gct tcc cac cca agt cga gag aag ccc ttt			918
Asn Cys Val Thr Glu Leu Ala Ser His Pro Ser Arg Glu Lys Pro Phe			

300	305	310	
gaa gac ttc ctc cca tcg cat tat aat tat ctg cag ttt gcc tac tat			966
Glu Asp Phe Leu Pro Ser His Tyr Asn Tyr Leu Gln Phe Ala Tyr Tyr			

315	320	325	
aac att ggg aat tat aca cag gct gtt gaa tgt gcc aag acc tat ctt			1014
Asn Ile Gly Asn Tyr Thr Gln Ala Val Glu Cys Ala Lys Thr Tyr Leu			

ctc ttc ttc ccc aat gac gag gtg atg aac caa aat ttg gcc tat tat 1062

Leu Phe Phe Pro Asn Asp Glu Val Met Asn Gln Asn Leu Ala Tyr Tyr

330

335

340

gca gct atg ctt gga gaa gaa cac acc aga tcc atc ggc ccc cgt gag 1110

Ala Ala Met Leu Gly Glu Glu His Thr Arg Ser Ile Gly Pro Arg Glu

345

350

355

360

agt gcc aag gag tac cga cag cga agc cta ctg gaa aaa gaa ctg ctt 1158

Ser Ala Lys Glu Tyr Arg Gln Arg Ser Leu Leu Glu Lys Glu Leu Leu

365

370

375

ttc ttc gct tat gat gtt ttt gga att ccc ttt gtg gat ccg gat tca 1206

Phe Phe Ala Tyr Asp Val Phe Gly Ile Pro Phe Val Asp Pro Asp Ser

380

385

390

tgg act cca gaa gaa gtg att ccc aag aga ttg caa gag aaa cag aag 1254

Trp Thr Pro Glu Glu Val Ile Pro Lys Arg Leu Gln Glu Lys Gln Lys

395

400

405

tca gaa cgg gaa aca gcc gta cgc atc tcc cag gag att ggg aac ctt 1302

Ser Glu Arg Glu Thr Ala Val Arg Ile Ser Gln Glu Ile Gly Asn Leu

410

415

420

atg aag gaa atc gag acc ctt gtg gaa gag aag acc aag gag tca ctg 1350

Met Lys Glu Ile Glu Thr Leu Val Glu Glu Lys Thr Lys Glu Ser Leu

425

430

435

440

gat gtg agc aga ctg acc cgg gaa ggt ggc ccc ctg ctg tat gaa ggc 1398

Asp Val Ser Arg Leu Thr Arg Glu Gly Gly Pro Leu Leu Tyr Glu Gly

445

450

455

atc agt ctc acc atg aac tcc aaa ctc ctg aat ggt tcc cag cgg gtg 1446

Ile Ser Leu Thr Met Asn Ser Lys Leu Leu Asn Gly Ser Gln Arg Val

460

465

470

gtg atg gac ggc gta atc tct gac cac gag tgt cag gag ctg cag aga 1494

Val Met Asp Gly Val Ile Ser Asp His Glu Cys Gln Glu Leu Gln Arg

475

480

485

ctg acc aat gtg gca gca acc tca gga gat ggc tac cgg ggt cag acc 1542

Leu Thr Asn Val Ala Ala Thr Ser Gly Asp Gly Tyr Arg Gly Gln Thr

490

495

500

tcc cca cat act ccc aat gaa aag ttc tat ggt gtc act gtc ttc aaa 1590

Ser Pro His Thr Pro Asn Glu Lys Phe Tyr Gly Val Thr Val Phe Lys

505

510

515

520

gcc ctc aag ctg ggg caa gaa ggc aaa gtt cct ctg cag agt gcc cac 1638

Ala Leu Lys Leu Gly Gln Glu Gly Lys Val Pro Leu Gln Ser Ala His

525

530

535

ctg tac tac aac gtg acg gag aag gtg cgg cgc atc atg gag tcc tac 1686

Leu Tyr Tyr Asn Val Thr Glu Lys Val Arg Arg Ile Met Glu Ser Tyr

540

545

550

ttc cgc ctg gat acg ccc ctc tac ttt tcc tac tct cat ctg gtg tgc 1734

Phe Arg Leu Asp Thr Pro Leu Tyr Phe Ser Tyr Ser His Leu Val Cys
 555 560 565

cgc act gcc atc gaa gag gtc cag gca gag agg aag gat gat agt cat 1782
 Arg Thr Ala Ile Glu Glu Val Gln Ala Glu Arg Lys Asp Asp Ser His
 570 575 580

cca gtc cac gtg gac aac tgc atc ctg aat gcc gag acc ctc gtg tgt 1830
 Pro Val His Val Asp Asn Cys Ile Leu Asn Ala Glu Thr Leu Val Cys
 585 590 595 600

gtc aaa gag ccc cca gcc tac acc ttc cgc gac tac agc gcc atc ctt 1878
 Val Lys Glu Pro Pro Ala Tyr Thr Phe Arg Asp Tyr Ser Ala Ile Leu
 605 610 615

tac cta aat ggg gac ttc gat ggc gga aac ttt tat ttc act gaa ctg 1926
 Tyr Leu Asn Gly Asp Phe Asp Gly Gly Asn Phe Tyr Phe Thr Glu Leu
 620 625 630

gat gcc aag acc gtg acg gca gag gtg cag cct cag tgt gga aga gcc 1974
 Asp Ala Lys Thr Val Thr Ala Glu Val Gln Pro Gln Cys Gly Arg Ala
 635 640 645

gtg gga ttc tct tca ggc act gaa aac cca cat gga gtg aag gct gtc 2022
 Val Gly Phe Ser Ser Gly Thr Glu Asn Pro His Gly Val Lys Ala Val
 650 655 660

acc agg ggg cag cgc tgt gcc atc gcc ctg tgg ttc acc ctg gac cct 2070
 Thr Arg Gly Gln Arg Cys Ala Ile Ala Leu Trp Phe Thr Leu Asp Pro

665	670	675	680	
cga cac agc gag cgg gac agg gtg cag gca gat gac ctg gtg aag atg	2118			
Arg His Ser Glu Arg Asp Arg Val Gln Ala Asp Asp Leu Val Lys Met				
685	690	695		

ctc ttc agc cca gaa gag atg gac ctc tcc cag gag cag ccc ctg gat	2166	
Leu Phe Ser Pro Glu Glu Met Asp Leu Ser Gln Glu Gln Pro Leu Asp		
700	705	710

gcc cag cag ggc ccc ccc gaa cct gca caa gag tct ctc tca ggc agt	2214	
Ala Gln Gln Gly Pro Pro Glu Pro Ala Gln Glu Ser Leu Ser Gly Ser		
715	720	725

gaa tcg aag ccc aag gat gag cta tgacagcgtc caggtcagac ggatgggtga	2268
Glu Ser Lys Pro Lys Asp Glu Leu	
730	735

ctagacccat ggagaggaac tcttctgcac tctgagctgg ccagcccctc ggggctgcag	2328
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tgctactgct cttggagtgg acatgaccag acaccgcacc ccctggatct ggctgagggc	2448
tcaggacaca ggcccagcca cccccagggg cctccacagg ccgctgcata acagcgatac	2508
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<212> PRT

<213> Homo sapiens

<400> 114

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20 25 30

Val Thr Pro Asp Leu Leu Phe Ala Glu Gly Thr Ala Ala Tyr Ala Arg

35 40 45

Gly Asp Trp Pro Gly Val Val Leu Ser Met Glu Arg Ala Leu Arg Ser

50 55 60

Arg Ala Ala Leu Arg Ala Leu Arg Leu Arg Cys Arg Thr Gln Cys Ala

65 70 75 80

Ala Asp Phe Pro Trp Glu Leu Asp Pro Asp Trp Ser Pro Ser Pro Ala

85 90 95

Gln Ala Ser Gly Ala Ala Ala Leu Arg Asp Leu Ser Phe Phe Gly Gly

100 105 110

Leu Leu Arg Arg Ala Ala Cys Leu Arg Arg Cys Leu Gly Pro Pro Ala

115 120 125

Ala His Ser Leu Ser Glu Glu Met Glu Leu Glu Phe Arg Lys Arg Ser
130 135 140

Pro Tyr Asn Tyr Leu Gln Val Ala Tyr Phe Lys Ile Asn Lys Leu Glu
145 150 155 160

Lys Ala Val Ala Ala Ala His Thr Phe Phe Val Gly Asn Pro Glu His
165 170 175

Met Glu Met Gln Gln Asn Leu Asp Tyr Tyr Gln Thr Met Ser Gly Val
180 185 190

Lys Glu Ala Asp Phe Lys Asp Leu Glu Thr Gln Pro His Met Gln Glu
195 200 205

Phe Arg Leu Gly Val Arg Leu Tyr Ser Glu Glu Gln Pro Gln Glu Ala
210 215 220

Val Pro His Leu Glu Ala Ala Leu Gln Glu Tyr Phe Val Ala Tyr Glu
225 230 235 240

Glu Cys Arg Ala Leu Cys Glu Gly Pro Tyr Asp Tyr Asp Gly Tyr Asn
245 250 255

Tyr Leu Glu Tyr Asn Ala Asp Leu Phe Gln Ala Ile Thr Asp His Tyr
260 265 270

Ile Gln Val Leu Asn Cys Lys Gln Asn Cys Val Thr Glu Leu Ala Ser

275

280

285

His Pro Ser Arg Glu Lys Pro Phe Glu Asp Phe Leu Pro Ser His Tyr

290

295

300

Asn Tyr Leu Gln Phe Ala Tyr Tyr Asn Ile Gly Asn Tyr Thr Gln Ala

305

310

315

320

Val Glu Cys Ala Lys Thr Tyr Leu Leu Phe Phe Pro Asn Asp Glu Val

325

330

335

Met Asn Gln Asn Leu Ala Tyr Tyr Ala Ala Met Leu Gly Glu Glu His

340

345

350

Thr Arg Ser Ile Gly Pro Arg Glu Ser Ala Lys Glu Tyr Arg Gln Arg

355

360

365

Ser Leu Leu Glu Lys Glu Leu Leu Phe Phe Ala Tyr Asp Val Phe Gly

370

375

380

Ile Pro Phe Val Asp Pro Asp Ser Trp Thr Pro Glu Glu Val Ile Pro

385

390

395

400

Lys Arg Leu Gln Glu Lys Gln Lys Ser Glu Arg Glu Thr Ala Val Arg

405

410

415

Ile Ser Gln Glu Ile Gly Asn Leu Met Lys Glu Ile Glu Thr Leu Val

420

425

430

Glu Glu Lys Thr Lys Glu Ser Leu Asp Val Ser Arg Leu Thr Arg Glu
435 440 445

Gly Gly Pro Leu Leu Tyr Glu Gly Ile Ser Leu Thr Met Asn Ser Lys
450 455 460

Leu Leu Asn Gly Ser Gln Arg Val Val Met Asp Gly Val Ile Ser Asp
465 470 475 480

His Glu Cys Gln Glu Leu Gln Arg Leu Thr Asn Val Ala Ala Thr Ser
485 490 495

Gly Asp Gly Tyr Arg Gly Gln Thr Ser Pro His Thr Pro Asn Glu Lys
500 505 510

Phe Tyr Gly Val Thr Val Phe Lys Ala Leu Lys Leu Gly Gln Glu Gly
515 520 525

Lys Val Pro Leu Gln Ser Ala His Leu Tyr Tyr Asn Val Thr Glu Lys
530 535 540

Val Arg Arg Ile Met Glu Ser Tyr Phe Arg Leu Asp Thr Pro Leu Tyr
545 550 555 560

Phe Ser Tyr Ser His Leu Val Cys Arg Thr Ala Ile Glu Glu Val Gln
565 570 575

Ala Glu Arg Lys Asp Asp Ser His Pro Val His Val Asp Asn Cys Ile
580 585 590

Leu Asn Ala Glu Thr Leu Val Cys Val Lys Glu Pro Pro Ala Tyr Thr

595

600

605

Phe Arg Asp Tyr Ser Ala Ile Leu Tyr Leu Asn Gly Asp Phe Asp Gly

610

615

620

Gly Asn Phe Tyr Phe Thr Glu Leu Asp Ala Lys Thr Val Thr Ala Glu

625

630

635

640

Val Gln Pro Gln Cys Gly Arg Ala Val Gly Phe Ser Ser Gly Thr Glu

645

650

655

Asn Pro His Gly Val Lys Ala Val Thr Arg Gly Gln Arg Cys Ala Ile

660

665

670

Ala Leu Trp Phe Thr Leu Asp Pro Arg His Ser Glu Arg Asp Arg Val

675

680

685

Gln Ala Asp Asp Leu Val Lys Met Leu Phe Ser Pro Glu Glu Met Asp

690

695

700

Leu Ser Gln Glu Gln Pro Leu Asp Ala Gln Gln Gly Pro Pro Glu Pro

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710

715

720

Ala Gln Glu Ser Leu Ser Gly Ser Glu Ser Lys Pro Lys Asp Glu Leu

725

730

735



<210> 115

<211> 2179

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (56)..(1087)

<400> 115

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Phe Thr Ser Thr Gly Ser Ser Gly Leu Tyr Lys Ala Pro Leu Ser Lys

5

10

15

agc ctt ctg ctg gtc ccc agt gcc ctc tcc ctc ctg ctc gcc ctc ctc 154

Ser Leu Leu Leu Val Pro Ser Ala Leu Ser Leu Leu Leu Ala Leu Leu

20

25

30

ctg cct cac tgc cag aag ctc ttt gtg tat gac ctt cac gca gtc aag 202

Leu Pro His Cys Gln Lys Leu Phe Val Tyr Asp Leu His Ala Val Lys

35

40

45

aac gac ttc cag att tgg agg ttg ata tgt gga aga ata att tgc ctt 250

Asn Asp Phe Gln Ile Trp Arg Leu Ile Cys Gly Arg Ile Ile Cys Leu

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55

60

65

gat ttg aaa gat act ttc tgc agt agt ctg ctt att tat aat ttt agg 298

Asp Leu Lys Asp Thr Phe Cys Ser Ser Leu Leu Ile Tyr Asn Phe Arg

70

75

80

ata ttt gaa aga aga tat gga agc aga aaa ttt gca tcc ttt ttg ctg 346

Ile Phe Glu Arg Arg Tyr Gly Ser Arg Lys Phe Ala Ser Phe Leu Leu

85

90

95

ggt tcc tgg gtt ttg tca gcc tta ttt gac ttt ctc ctc att gaa gct 394

Gly Ser Trp Val Leu Ser Ala Leu Phe Asp Phe Leu Leu Ile Glu Ala

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atg cag tat ttc ttt ggc atc act gca gct agt aat ttg cct tct gga 442

Met Gln Tyr Phe Phe Gly Ile Thr Ala Ala Ser Asn Leu Pro Ser Gly

115

120

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ttc ctg gca cct gtg ttt gct ctg ttt gta cca ttt tac tgc tcc ata 490

Phe Leu Ala Pro Val Phe Ala Leu Phe Val Pro Phe Tyr Cys Ser Ile

130

135

140

145

cca aga gtc caa gtg gca caa att ctg ggt ccg ttg tcc atc aca aac 538

Pro Arg Val Gln Val Ala Gln Ile Leu Gly Pro Leu Ser Ile Thr Asn

150

155

160

aag aca ttg att tat ata ttg gga ctg cag ctt ttc acc tct ggt tcc 586

Lys Thr Leu Ile Tyr Ile Leu Gly Leu Gln Leu Phe Thr Ser Gly Ser

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170

175

tac atc tgg att gta gcc ata agt gga ctt atg tcc ggt ctg tgc tac 634

Tyr Ile Trp Ile Val Ala Ile Ser Gly Leu Met Ser Gly Leu Cys Tyr

180

185

190

gac agc aaa atg ttc cag gtg cat cag gtg ctc tgc atc ccc agc tgg 682

Asp Ser Lys Met Phe Gln Val His Gln Val Leu Cys Ile Pro Ser Trp

195

200

205

atg gca aaa ttc ttt tct tgg aca ctt gaa ccc atc ttc tct tct tca 730

Met Ala Lys Phe Phe Ser Trp Thr Leu Glu Pro Ile Phe Ser Ser Ser

210

215

220

225

gaa ccc acc agc gaa gcc aga att ggg atg gga gcc acg ctg gac atc 778

Glu Pro Thr Ser Glu Ala Arg Ile Gly Met Gly Ala Thr Leu Asp Ile

230

235

240

cag aga cag cag aga atg gag ctg ctg gac cgg cag ctg atg ttc tct 826

Gln Arg Gln Gln Arg Met Glu Leu Leu Asp Arg Gln Leu Met Phe Ser

245

250

255

cag ttt gca caa ggg agg cga cag aga cag cag cag gga gga atg atc 874

Gln Phe Ala Gln Gly Arg Arg Gln Arg Gln Gln Gln Gly Gly Met Ile

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265

270

aat tgg aat cgt ctt ttt cct cct tta cgt cag cga caa aac gta aac 922

Asn Trp Asn Arg Leu Phe Pro Pro Leu Arg Gln Arg Gln Asn Val Asn

275

280

285

tat cag ggc ggt cgg cag tct gag cca gca gcg ccc cct cta gaa gtt 970

Tyr Gln Gly Gly Arg Gln Ser Glu Pro Ala Ala Pro Pro Leu Glu Val
290 295 300 305

tct gag gaa cag gtc gcc cgg ctc atg gag atg gga ttt tcc aga ggt 1018
Ser Glu Glu Gln Val Ala Arg Leu Met Glu Met Gly Phe Ser Arg Gly
310 315 320

gat gct ttg gaa gcc ctg aga gct tca aac aat gac ctc aat gtc gcc 1066
Asp Ala Leu Glu Ala Leu Arg Ala Ser Asn Asn Asp Leu Asn Val Ala
325 330 335

acc aac ttc ctg ctg cag cac tgatagtcac aggccaacac tgggaccgga 1117
Thr Asn Phe Leu Leu Gln His
340

ccggcagccg agtgacagtg cgtgggtcccc accatcagat cagcccgggg accgagcatc 1177

tctggtgctg atgttcttgt gggaagaggg aggttccacc gcacccctgc cctcaaccgc 1237

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actcttgcaa tgtgcaactg ttatgttctg caaatgagc aacgatgtat caaattgatg 2137

caaatttaga tgttgatact tacaataaag tttttaatgt gt 2179

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<211> 344

<212> PRT

<213> Homo sapiens

<400> 116

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Lys Ser Leu Leu Leu Val Pro Ser Ala Leu Ser Leu Leu Leu Ala Leu

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Leu Leu Pro His Cys Gln Lys Leu Phe Val Tyr Asp Leu His Ala Val

35 40 45

Lys Asn Asp Phe Gln Ile Trp Arg Leu Ile Cys Gly Arg Ile Ile Cys

50 55 60

Leu Asp Leu Lys Asp Thr Phe Cys Ser Ser Leu Leu Ile Tyr Asn Phe

65 70 75 80

Arg Ile Phe Glu Arg Arg Tyr Gly Ser Arg Lys Phe Ala Ser Phe Leu

85 90 95

Leu Gly Ser Trp Val Leu Ser Ala Leu Phe Asp Phe Leu Leu Ile Glu

100 105 110

Ala Met Gln Tyr Phe Phe Gly Ile Thr Ala Ala Ser Asn Leu Pro Ser

115 120 125

Gly Phe Leu Ala Pro Val Phe Ala Leu Phe Val Pro Phe Tyr Cys Ser

130 135 140

Ile Pro Arg Val Gln Val Ala Gln Ile Leu Gly Pro Leu Ser Ile Thr

145 150 155 160

Asn Lys Thr Leu Ile Tyr Ile Leu Gly Leu Gln Leu Phe Thr Ser Gly
165 170 175

Ser Tyr Ile Trp Ile Val Ala Ile Ser Gly Leu Met Ser Gly Leu Cys
180 185 190

Tyr Asp Ser Lys Met Phe Gln Val His Gln Val Leu Cys Ile Pro Ser
195 200 205

Trp Met Ala Lys Phe Phe Ser Trp Thr Leu Glu Pro Ile Phe Ser Ser
210 215 220

Ser Glu Pro Thr Ser Glu Ala Arg Ile Gly Met Gly Ala Thr Leu Asp
225 230 235 240

Ile Gln Arg Gln Gln Arg Met Glu Leu Leu Asp Arg Gln Leu Met Phe
245 250 255

Ser Gln Phe Ala Gln Gly Arg Arg Gln Arg Gln Gln Gln Gly Gly Met
260 265 270

Ile Asn Trp Asn Arg Leu Phe Pro Pro Leu Arg Gln Arg Gln Asn Val
275 280 285

Asn Tyr Gln Gly Gly Arg Gln Ser Glu Pro Ala Ala Pro Pro Leu Glu
290 295 300

Val Ser Glu Glu Gln Val Ala Arg Leu Met Glu Met Gly Phe Ser Arg

305

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320

Gly Asp Ala Leu Glu Ala Leu Arg Ala Ser Asn Asn Asp Leu Asn Val

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330

335

Ala Thr Asn Phe Leu Leu Gln His

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<210> 117

<211> 3362

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (206)..(829)

<400> 117

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ggcgccggct gcgcagagga gccgctctcg ccgccgccac ctcggctggg agcccacgag 180

gctgccgcat cctgccctcg gaaca atg gga ctc ggc gcg cga ggt gct tgg 232

Met Gly Leu Gly Ala Arg Gly Ala Trp

1

5

gcc gcg ctg ctc ctg ggg acg ctg cag gtg cta gcg ctg ctg ggg gcc 280
 Ala Ala Leu Leu Leu Gly Thr Leu Gln Val Leu Ala Leu Leu Gly Ala
 10 15 20 25

gcc cat gaa agc gca gcc atg gcg gca tct gca aac ata gag aat tct 328
 Ala His Glu Ser Ala Ala Met Ala Ala Ser Ala Asn Ile Glu Asn Ser

30

35

40

ggg ctt cca cac aac tcc agt gct aac tca aca gag act ctc caa cat 376
 Gly Leu Pro His Asn Ser Ser Ala Asn Ser Thr Glu Thr Leu Gln His
 45 50 55

gtg cct tct gac cat aca aat gaa act tcc aac agt act gtg aaa cca 424
 Val Pro Ser Asp His Thr Asn Glu Thr Ser Asn Ser Thr Val Lys Pro
 60 65 70

cca act tca gtt gcc tca gac tcc agt aat aca acg gtc acc acc atg 472
 Pro Thr Ser Val Ala Ser Asp Ser Ser Asn Thr Thr Val Thr Thr Met
 75 80 85

aaa cct aca gcg gca tct aat aca aca aca cca ggg atg gtc tca aca 520
 Lys Pro Thr Ala Ala Ser Asn Thr Thr Thr Pro Gly Met Val Ser Thr
 90 95 100 105

aat atg act tct acc acc tta aag tct aca ccc aaa aca aca agt gtt 568
 Asn Met Thr Ser Thr Thr Leu Lys Ser Thr Pro Lys Thr Thr Ser Val
 110 115 120

tca cag aac aca tct cag ata tca aca tcc aca atg acc gta acc cac 616

Ser Gln Asn Thr Ser Gln Ile Ser Thr Ser Thr Met Thr Val Thr His
 125 130 135

aat agt tca gtg aca tct gct gct tca tca gta aca atc aca aca act 664
 Asn Ser Ser Val Thr Ser Ala Ala Ser Ser Val Thr Ile Thr Thr Thr
 140 145 150

atg cat tct gaa gca aag aaa gga tca aaa ttt gat act ggg agc ttt 712
 Met His Ser Glu Ala Lys Lys Gly Ser Lys Phe Asp Thr Gly Ser Phe
 155 160 165

gtt ggt ggt att gta tta acg ctg gga gtt tta tct att ctt tac att 760
 Val Gly Gly Ile Val Leu Thr Leu Gly Val Leu Ser Ile Leu Tyr Ile
 170 175 180 185

gga tgc aaa atg tat tac tca aga aga ggc att cgg tat cga acc ata 808
 Gly Cys Lys Met Tyr Tyr Ser Arg Arg Gly Ile Arg Tyr Arg Thr Ile
 190 195 200

gat gaa cat gat gcc atc att taaggaaatc catggaccaa ggatggaata 859
 Asp Glu His Asp Ala Ile Ile
 205

cagattgatg ctgccctatc aattaatttt ggttttattaa tagttttaaaa caatattctc 919

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<210> 118

<211> 208

<212> PRT

<213> Homo sapiens

<400> 118

Met Gly Leu Gly Ala Arg Gly Ala Trp Ala Ala Leu Leu Leu Gly Thr

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15

Leu Gln Val Leu Ala Leu Leu Gly Ala Ala His Glu Ser Ala Ala Met

20

25

30

Ala Ala Ser Ala Asn Ile Glu Asn Ser Gly Leu Pro His Asn Ser Ser

35

40

45

Ala Asn Ser Thr Glu Thr Leu Gln His Val Pro Ser Asp His Thr Asn

50

55

60

Glu Thr Ser Asn Ser Thr Val Lys Pro Pro Thr Ser Val Ala Ser Asp

65

70

75

80

Ser Ser Asn Thr Thr Val Thr Thr Met Lys Pro Thr Ala Ala Ser Asn

85

90

95

Thr Thr Thr Pro Gly Met Val Ser Thr Asn Met Thr Ser Thr Thr Leu

100

105

110

Lys Ser Thr Pro Lys Thr Thr Ser Val Ser Gln Asn Thr Ser Gln Ile

115

120

125

Ser Thr Ser Thr Met Thr Val Thr His Asn Ser Ser Val Thr Ser Ala

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135

140

Ala Ser Ser Val Thr Ile Thr Thr Thr Met His Ser Glu Ala Lys Lys

145

150

155

160

Gly Ser Lys Phe Asp Thr Gly Ser Phe Val Gly Gly Ile Val Leu Thr

165

170

175

Leu Gly Val Leu Ser Ile Leu Tyr Ile Gly Cys Lys Met Tyr Tyr Ser

180

185

190

Arg Arg Gly Ile Arg Tyr Arg Thr Ile Asp Glu His Asp Ala Ile Ile

195

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<222> (180)..(1226)

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agacgttctc cttggaagct cttggccctg aggactttgc ctggggcatt ggccctgcc 179

atg gcg ttc cgg agg gcc gag ggc acg tct atg atc cag gcc ctg gcc 227

Met Ala Phe Arg Arg Ala Glu Gly Thr Ser Met Ile Gln Ala Leu Ala

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atg acg gtg gcc gag atc ccc gtg ttc ctg tac acg acg ttt ggg cag 275

Met Thr Val Ala Glu Ile Pro Val Phe Leu Tyr Thr Thr Phe Gly Gln

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tct gca ttc tcc cag cta cgg ttg acg cca ggc ctg cgg aaa gtc ctc 323

Ser Ala Phe Ser Gln Leu Arg Leu Thr Pro Gly Leu Arg Lys Val Leu

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ttt gcc acg gcc ctg ggg act gtg gcc ctg gcc ctg gct gcc cac cag 371

Phe Ala Thr Ala Leu Gly Thr Val Ala Leu Ala Leu Ala Ala His Gln

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ctg aag agg cga cgg agg agg aag aag cag gtt ggt ccc gag atg gga 419

Leu Lys Arg Arg Arg Arg Arg Lys Lys Gln Val Gly Pro Glu Met Gly

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ggg gag cag ctg ggc acg gtg ccc ctc cct atc ctc ttg gcc agg aag 467

Gly Glu Gln Leu Gly Thr Val Pro Leu Pro Ile Leu Leu Ala Arg Lys

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gtc cct tca gtg aag aaa gga tac tcc agc cgg aga gtc cag agc ccc 515

Val Pro Ser Val Lys Lys Gly Tyr Ser Ser Arg Arg Val Gln Ser Pro

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agc agc aag agc aac gac acc ctg agt ggc atc tct tcc att gag ccc 563

Ser Ser Lys Ser Asn Asp Thr Leu Ser Gly Ile Ser Ser Ile Glu Pro

115

120

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agc aag cac tcg ggc tcc tcc cac agt gtg gcc tcg atg atg gca gtg 611

Ser Lys His Ser Gly Ser Ser His Ser Val Ala Ser Met Met Ala Val
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aac tca tcc agc ccc aca gcc gcg tgc tcg gga cta tgg gat gcc aga 659
Asn Ser Ser Ser Pro Thr Ala Ala Cys Ser Gly Leu Trp Asp Ala Arg
145 150 155 160

ggg atg gag gag tct ctg acc acc agc gac ggc aat gca gag agc ctg 707
Gly Met Glu Glu Ser Leu Thr Thr Ser Asp Gly Asn Ala Glu Ser Leu
165 170 175

tac atg caa ggc atg gag ctg ttt gag gaa gct ctg cag aag tgg gag 755
Tyr Met Gln Gly Met Glu Leu Phe Glu Glu Ala Leu Gln Lys Trp Glu
180 185 190

cag gca cta agc gtg ggc cag cgg ggg gac agc ggc agc acc ccc atg 803
Gln Ala Leu Ser Val Gly Gln Arg Gly Asp Ser Gly Ser Thr Pro Met
195 200 205

ccc agg gac ggc ctc cgg aac cca gag act gca tca gag cca ctg tct 851
Pro Arg Asp Gly Leu Arg Asn Pro Glu Thr Ala Ser Glu Pro Leu Ser
210 215 220

gag cca gag tca cag cgg aag gag ttt gca gag aag ctg gag tcc ctg 899
Glu Pro Glu Ser Gln Arg Lys Glu Phe Ala Glu Lys Leu Glu Ser Leu
225 230 235 240

ctg cac cgt gcc tac cac ctg cag gag gag ttc ggc tcc acc ttc ccc 947
Leu His Arg Ala Tyr His Leu Gln Glu Glu Phe Gly Ser Thr Phe Pro

245

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gca gac agc atg ctg cta gac ctc gag agg acc ctc atg ctg ccc ctg 995

Ala Asp Ser Met Leu Leu Asp Leu Glu Arg Thr Leu Met Leu Pro Leu

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acc gag ggc tcg ctg cgg ctg cgg gcg gac gat gag gac agc ctg act 1043

Thr Glu Gly Ser Leu Arg Leu Arg Ala Asp Asp Glu Asp Ser Leu Thr

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tca gag gat tcc ttc ttc tcc gcc acc gag ctc ttt gag tcc ctg cag 1091

Ser Glu Asp Ser Phe Phe Ser Ala Thr Glu Leu Phe Glu Ser Leu Gln

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act gga gat tac ccg atc cca ctc tcc aga ccc gcc gct gcc tat gag 1139

Thr Gly Asp Tyr Pro Ile Pro Leu Ser Arg Pro Ala Ala Ala Tyr Glu

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gag gcc ctg cag ctg gtg aag gag ggg aga gtg cct tgc cgg acc ctc 1187

Glu Ala Leu Gln Leu Val Lys Glu Gly Arg Val Pro Cys Arg Thr Leu

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aga gcc cca aag gct tcc tgg aga gct acg agg aga tgc tgagctatgc 1236

Arg Ala Pro Lys Ala Ser Trp Arg Ala Thr Arg Arg Cys

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agtcgaataa acaattgaga cg 3598

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Ser Ala Phe Ser Gln Leu Arg Leu Thr Pro Gly Leu Arg Lys Val Leu
35 40 45

Phe Ala Thr Ala Leu Gly Thr Val Ala Leu Ala Leu Ala Ala His Gln
50 55 60

Leu Lys Arg Arg Arg Arg Arg Lys Lys Gln Val Gly Pro Glu Met Gly
65 70 75 80

Gly Glu Gln Leu Gly Thr Val Pro Leu Pro Ile Leu Leu Ala Arg Lys
85 90 95

Val Pro Ser Val Lys Lys Gly Tyr Ser Ser Arg Arg Val Gln Ser Pro
100 105 110

Ser Ser Lys Ser Asn Asp Thr Leu Ser Gly Ile Ser Ser Ile Glu Pro
115 120 125

Ser Lys His Ser Gly Ser Ser His Ser Val Ala Ser Met Met Ala Val
130 135 140

Asn Ser Ser Ser Pro Thr Ala Ala Cys Ser Gly Leu Trp Asp Ala Arg
145 150 155 160

Gly Met Glu Glu Ser Leu Thr Thr Ser Asp Gly Asn Ala Glu Ser Leu
165 170 175

Tyr Met Gln Gly Met Glu Leu Phe Glu Glu Ala Leu Gln Lys Trp Glu

180

185

190

Gln Ala Leu Ser Val Gly Gln Arg Gly Asp Ser Gly Ser Thr Pro Met

195

200

205

Pro Arg Asp Gly Leu Arg Asn Pro Glu Thr Ala Ser Glu Pro Leu Ser

210

215

220

Glu Pro Glu Ser Gln Arg Lys Glu Phe Ala Glu Lys Leu Glu Ser Leu

225

230

235

240

Leu His Arg Ala Tyr His Leu Gln Glu Glu Phe Gly Ser Thr Phe Pro

245

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Ala Asp Ser Met Leu Leu Asp Leu Glu Arg Thr Leu Met Leu Pro Leu

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270

Thr Glu Gly Ser Leu Arg Leu Arg Ala Asp Asp Glu Asp Ser Leu Thr

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280

285

Ser Glu Asp Ser Phe Phe Ser Ala Thr Glu Leu Phe Glu Ser Leu Gln

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Thr Gly Asp Tyr Pro Ile Pro Leu Ser Arg Pro Ala Ala Ala Tyr Glu

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Arg Ala Pro Lys Ala Ser Trp Arg Ala Thr Arg Arg Cys

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Met Ser Leu Thr Tyr Ile Leu Val Ala Leu Ala Ala Val Leu Leu Asn

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aac gtc ctg gtg gag aga ctg acc ctg cac acc agg atc acc gca ggc 155

Asn Val Leu Val Glu Arg Leu Thr Leu His Thr Arg Ile Thr Ala Gly

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tac ctc tta gcc ttg ggc cct ctc ctt ttt atc agc atc tgc gac gtg 203

Tyr Leu Leu Ala Leu Gly Pro Leu Leu Phe Ile Ser Ile Cys Asp Val

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tgg ctg cag ctc ttc tct cgg gac cag gcc tac gcc atc aac ctg gcc 251

Trp Leu Gln Leu Phe Ser Arg Asp Gln Ala Tyr Ala Ile Asn Leu Ala

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gct gtg ggc acc gtg gcc ttc ggc tgc aca gtg cag caa tcc agc ttc 299

Ala Val Gly Thr Val Ala Phe Gly Cys Thr Val Gln Gln Ser Ser Phe

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75

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tac ggg tac acg ggg atg ctg ccc aag cgg tac acg cag ggg gtg atg 347

Tyr Gly Tyr Thr Gly Met Leu Pro Lys Arg Tyr Thr Gln Gly Val Met

85

90

95

acc ggg gag agc acg gcg ggc gtg atg atc tct ctg agc cgc atc ctc 395

Thr Gly Glu Ser Thr Ala Gly Val Met Ile Ser Leu Ser Arg Ile Leu

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acg aag ctg ctg ctg ccc gac gag cgc gcc agc acg ctc atc ttc ttc 443

Thr Lys Leu Leu Leu Pro Asp Glu Arg Ala Ser Thr Leu Ile Phe Phe

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125

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Leu Val Ser Val Ala Leu Glu Leu Leu Cys Phe Leu Leu His Leu Leu

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gtg cgg cgc agc cgc ttc gtg ctc ttc cat acc aca cgg ccg cgt gac 539

Val Arg Arg Ser Arg Phe Val Leu Phe His Thr Thr Arg Pro Arg Asp

145

150

155

160

agc cac cgg ggc agg cca ggc ctg ggc agg ggc tat ggc tac cgc gtg 587

Ser His Arg Gly Arg Pro Gly Leu Gly Arg Gly Tyr Gly Tyr Arg Val

165

170

175

cac cac gac gtt gtc gcc ggg gac gtc cac ttc gag cac cca gcc ccg 635

His His Asp Val Val Ala Gly Asp Val His Phe Glu His Pro Ala Pro

180

185

190

gcc ctg gcc ccc aac gag tcc cca aag gac agc cca gcc cac gag gtg 683

Ala Leu Ala Pro Asn Glu Ser Pro Lys Asp Ser Pro Ala His Glu Val

195

200

205

acc ggc agc ggt ggg gcc tac atg cgc ttt gat gtg ccg cgg cca agg 731

Thr Gly Ser Gly Gly Ala Tyr Met Arg Phe Asp Val Pro Arg Pro Arg

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gtc cag cgc agc tgg ccc acc ttc aga gcc ctg tta ctg cac cgc tac 779

Val Gln Arg Ser Trp Pro Thr Phe Arg Ala Leu Leu Leu His Arg Tyr

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gtg gtg gcg cgg gtg atc tgg gcc gac atg ctc tcc atc gcc gtg acc 827

Val Val Ala Arg Val Ile Trp Ala Asp Met Leu Ser Ile Ala Val Thr

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tac ttc atc acg ctg tgc ctg ttc ccc ggc ctc gag tct gag atc cgc 875

Tyr Phe Ile Thr Leu Cys Leu Phe Pro Gly Leu Glu Ser Glu Ile Arg

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270

cac tgc atc ctg ggc gag tgg ctg ccc atc ctc atc atg gct gtg ttc 923

His Cys Ile Leu Gly Glu Trp Leu Pro Ile Leu Ile Met Ala Val Phe
 275 280 285

aac ctg tca gac ttc gtg ggc aag atc ctg gca gcc ctg ccc gtg gac 971
 Asn Leu Ser Asp Phe Val Gly Lys Ile Leu Ala Ala Leu Pro Val Asp
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tgg cgg ggc acc cac ctg ctg gcc tgc tcc tgc ctg cgt gtg gtc ttc 1019
 Trp Arg Gly Thr His Leu Leu Ala Cys Ser Cys Leu Arg Val Val Phe
 305 310 315 320

atc ccc ctc ttc atc ctg tgc gtc tac ccc agc ggc atg ccc gcc ctc 1067
 Ile Pro Leu Phe Ile Leu Cys Val Tyr Pro Ser Gly Met Pro Ala Leu
 325 330 335

cgt cac ccc gcc tgg ccc tgc atc ttc tca ctg ctc atg ggc atc agc 1115
 Arg His Pro Ala Trp Pro Cys Ile Phe Ser Leu Leu Met Gly Ile Ser
 340 345 350

aac ggc tac ttc ggc agc gtg ccc atg atc ctg gcg gca ggc aaa gtg 1163
 Asn Gly Tyr Phe Gly Ser Val Pro Met Ile Leu Ala Ala Gly Lys Val
 355 360 365

agc ccc aag cag cgg gag ctg gca ggg aac acc atg acc gtg tcc tac 1211
 Ser Pro Lys Gln Arg Glu Leu Ala Gly Asn Thr Met Thr Val Ser Tyr
 370 375 380

atg tca ggg ctg acg ctg ggg tcc gcc gtg gcc tac tgc acc tac agc 1259
 Met Ser Gly Leu Thr Leu Gly Ser Ala Val Ala Tyr Cys Thr Tyr Ser

385

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395

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ctc acc cgc gac gct cac ggc agc tgc ctg cac gcc tcc acc gcc aat 1307

Leu Thr Arg Asp Ala His Gly Ser Cys Leu His Ala Ser Thr Ala Asn

405

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415

ggt tcc atc ctc gca ggc ctc tgagccagcc ccgcccactg ccaggacgc 1358

Gly Ser Ile Leu Ala Gly Leu

420

cgagggcctg accagggggcc ccgagggcctg agggcccctc ccctgtcccc acctcagtgc 1418

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ggcagaccgc tgc 2451

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<212> PRT

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<400> 122

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20 25 30

Tyr Leu Leu Ala Leu Gly Pro Leu Leu Phe Ile Ser Ile Cys Asp Val
35 40 45

Trp Leu Gln Leu Phe Ser Arg Asp Gln Ala Tyr Ala Ile Asn Leu Ala
50 55 60

Ala Val Gly Thr Val Ala Phe Gly Cys Thr Val Gln Gln Ser Ser Phe
65 70 75 80

Tyr Gly Tyr Thr Gly Met Leu Pro Lys Arg Tyr Thr Gln Gly Val Met
85 90 95

Thr Gly Glu Ser Thr Ala Gly Val Met Ile Ser Leu Ser Arg Ile Leu
100 105 110

Thr Lys Leu Leu Leu Pro Asp Glu Arg Ala Ser Thr Leu Ile Phe Phe
115 120 125

Leu Val Ser Val Ala Leu Glu Leu Leu Cys Phe Leu Leu His Leu Leu
130 135 140

Val Arg Arg Ser Arg Phe Val Leu Phe His Thr Thr Arg Pro Arg Asp
145 150 155 160

Ser His Arg Gly Arg Pro Gly Leu Gly Arg Gly Tyr Gly Tyr Arg Val
165 170 175

His His Asp Val Val Ala Gly Asp Val His Phe Glu His Pro Ala Pro
180 185 190

Ala Leu Ala Pro Asn Glu Ser Pro Lys Asp Ser Pro Ala His Glu Val
195 200 205

Thr Gly Ser Gly Gly Ala Tyr Met Arg Phe Asp Val Pro Arg Pro Arg
210 215 220

Val Gln Arg Ser Trp Pro Thr Phe Arg Ala Leu Leu Leu His Arg Tyr
225 230 235 240

Val Val Ala Arg Val Ile Trp Ala Asp Met Leu Ser Ile Ala Val Thr
245 250 255

Tyr Phe Ile Thr Leu Cys Leu Phe Pro Gly Leu Glu Ser Glu Ile Arg
260 265 270

His Cys Ile Leu Gly Glu Trp Leu Pro Ile Leu Ile Met Ala Val Phe
275 280 285

Asn Leu Ser Asp Phe Val Gly Lys Ile Leu Ala Ala Leu Pro Val Asp
290 295 300

Trp Arg Gly Thr His Leu Leu Ala Cys Ser Cys Leu Arg Val Val Phe
305 310 315 320

Ile Pro Leu Phe Ile Leu Cys Val Tyr Pro Ser Gly Met Pro Ala Leu

325

330

335

Arg His Pro Ala Trp Pro Cys Ile Phe Ser Leu Leu Met Gly Ile Ser

340

345

350

Asn Gly Tyr Phe Gly Ser Val Pro Met Ile Leu Ala Ala Gly Lys Val

355

360

365

Ser Pro Lys Gln Arg Glu Leu Ala Gly Asn Thr Met Thr Val Ser Tyr

370

375

380

Met Ser Gly Leu Thr Leu Gly Ser Ala Val Ala Tyr Cys Thr Tyr Ser

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Leu Thr Arg Asp Ala His Gly Ser Cys Leu His Ala Ser Thr Ala Asn

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Gly Ser Ile Leu Ala Gly Leu

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<210> 123

<211> 2518

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (29)..(1693)

<400> 123

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Thr His Leu Glu Val Ala Arg Gly Lys Arg Ala Ala Leu Phe Phe Ala

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15

20

gcg gtg gcc atc gtg ctg ggg cta ccg ctc tgg tgg aag acc acg gag 148

Ala Val Ala Ile Val Leu Gly Leu Pro Leu Trp Trp Lys Thr Thr Glu

25

30

35

40

acc tac cgg gcc tcg ttg cct tac tcc cag atc agt ggc ctg aat gcc 196

Thr Tyr Arg Ala Ser Leu Pro Tyr Ser Gln Ile Ser Gly Leu Asn Ala

45

50

55

ctt cag ctc cgc ctc atg gtg cct gtc act gtc gtg ttt acg cgg gag 244

Leu Gln Leu Arg Leu Met Val Pro Val Thr Val Val Phe Thr Arg Glu

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65

70

tca gtg ccc ctg gac gac cag gag aag ctg ccc ttc acc gtt gtg cat 292

Ser Val Pro Leu Asp Asp Gln Glu Lys Leu Pro Phe Thr Val Val His

75

80

85

gaa aga gag att cct ctg aaa tac aaa atg aaa atc aaa tgc cgt ttc 340

Glu Arg Glu Ile Pro Leu Lys Tyr Lys Met Lys Ile Lys Cys Arg Phe

90

95

100

cag aag gcc tat cgg agg gct ttg gac cat gag gag gag gcc ctg tca 388

Gln Lys Ala Tyr Arg Arg Ala Leu Asp His Glu Glu Glu Ala Leu Ser

105 110 115 120

tcg ggc agt gtg caa gag gca gaa gcc atg tta gat gag cct cag gaa 436

Ser Gly Ser Val Gln Glu Ala Glu Ala Met Leu Asp Glu Pro Gln Glu

125 130 135

caa gcg gag ggc tcc ctg act gtg tac gtg ata tct gaa cac tcc tca 484

Gln Ala Glu Gly Ser Leu Thr Val Tyr Val Ile Ser Glu His Ser Ser

140 145 150

ctt ctt ccc cag gac atg atg agc tac att ggg ccc aag agg aca gca 532

Leu Leu Pro Gln Asp Met Met Ser Tyr Ile Gly Pro Lys Arg Thr Ala

155 160 165

gtg gtg cgg ggg ata atg cac cgg gag gcc ttt aac atc att ggc cgc 580

Val Val Arg Gly Ile Met His Arg Glu Ala Phe Asn Ile Ile Gly Arg

170 175 180

cgc ata gtc cag gtg gcc cag gcc atg tct ttg act gag gat gtg ctt 628

Arg Ile Val Gln Val Ala Gln Ala Met Ser Leu Thr Glu Asp Val Leu

185 190 195 200

gct gct gct ctg gct gac cac ctt cca gag gac aag tgg agc gct gag 676

Ala Ala Ala Leu Ala Asp His Leu Pro Glu Asp Lys Trp Ser Ala Glu

205 210 215

aag agg cgg cct ctc aag tcc agc ttg ggc tat gag atc acc ttc agt 724

Lys Arg Arg Pro Leu Lys Ser Ser Leu Gly Tyr Glu Ile Thr Phe Ser

220

225

230

tta ctc aac cca gac ccc aag tcc cat gat gtc tac tgg gac att gag 772

Leu Leu Asn Pro Asp Pro Lys Ser His Asp Val Tyr Trp Asp Ile Glu

235

240

245

ggg gct gtc cgg cgc tat gtg caa cct tcc ctg aat gcc ctc ggt gcc 820

Gly Ala Val Arg Arg Tyr Val Gln Pro Ser Leu Asn Ala Leu Gly Ala

250

255

260

gct ggc aac ttc tct gtg gac tct cag att ctt tac tat gca atg ttg 868

Ala Gly Asn Phe Ser Val Asp Ser Gln Ile Leu Tyr Tyr Ala Met Leu

265

270

275

280

ggg gtg aat ccc cgc ttt gac tca gct tcc tcc agc tac tat ttg gac 916

Gly Val Asn Pro Arg Phe Asp Ser Ala Ser Ser Ser Tyr Tyr Leu Asp

285

290

295

atg cac agc ctc ccc cat gtc atc aac cca gtg gag tcc cgg ctg gga 964

Met His Ser Leu Pro His Val Ile Asn Pro Val Glu Ser Arg Leu Gly

300

305

310

tcc agt gct gcc tcc ttg tac cct gtg ctc aac ttt cta ctc tac gtg 1012

Ser Ser Ala Ala Ser Leu Tyr Pro Val Leu Asn Phe Leu Leu Tyr Val

315

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cct gag ctt gca cac tca ccg ctg tac att cag gac aag gat ggc gct 1060

Pro Glu Leu Ala His Ser Pro Leu Tyr Ile Gln Asp Lys Asp Gly Ala
330 335 340

cca gtg gcc acc aat gcc ttc cat agt ccc cgc tgg ggt ggc att atg 1108
Pro Val Ala Thr Asn Ala Phe His Ser Pro Arg Trp Gly Gly Ile Met
345 350 355 360

gta tat aat gtt gac tcc aaa acc tat aat gcc tca gtg ctg cca gtg 1156
Val Tyr Asn Val Asp Ser Lys Thr Tyr Asn Ala Ser Val Leu Pro Val
365 370 375

aga gtc gag gtg gac atg gtg cga gtg atg gag gtg ttc ctg gca cag 1204
Arg Val Glu Val Asp Met Val Arg Val Met Glu Val Phe Leu Ala Gln
380 385 390

ttg cgg ttg ctc ttt ggg att gct cag ccc cag ctg cct cca aaa tgc 1252
Leu Arg Leu Leu Phe Gly Ile Ala Gln Pro Gln Leu Pro Pro Lys Cys
395 400 405

ctg ctt tca ggg cct acg agt gaa ggg cta atg acc tgg gag cta gac 1300
Leu Leu Ser Gly Pro Thr Ser Glu Gly Leu Met Thr Trp Glu Leu Asp
410 415 420

cgg ctg ctc tgg gct cgg tca gtg gag aac ctg gcc aca gcc acc acc 1348
Arg Leu Leu Trp Ala Arg Ser Val Glu Asn Leu Ala Thr Ala Thr Thr
425 430 435 440

acc ctt acc tcc ctg gcg cag ctt ctg ggc aag atc agc aac att gtc 1396
Thr Leu Thr Ser Leu Ala Gln Leu Leu Gly Lys Ile Ser Asn Ile Val

445

450

455

att aag gac gac gtg gca tct gag gtg tac aag gct gta gct gcc gtc 1444

Ile Lys Asp Asp Val Ala Ser Glu Val Tyr Lys Ala Val Ala Ala Val

460

465

470

cag aag tcg gca gaa gag ttg gcg tct ggg cac ctg gca tct gcc ttt 1492

Gln Lys Ser Ala Glu Glu Leu Ala Ser Gly His Leu Ala Ser Ala Phe

475

480

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gtc gcc agc cag gaa gct gtg aca tcc tct gag ctt gcc ttc ttt gac 1540

Val Ala Ser Gln Glu Ala Val Thr Ser Ser Glu Leu Ala Phe Phe Asp

490

495

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ccg tca ctc ctc cac ctc ctt tat ttc cct gat tac cag aag ttt gcc 1588

Pro Ser Leu Leu His Leu Leu Tyr Phe Pro Asp Tyr Gln Lys Phe Ala

505

510

515

520

atc tac atc cca ctc ttc ctg cct atg gct gtg ccc atc ctc ctg tcc 1636

Ile Tyr Ile Pro Leu Phe Leu Pro Met Ala Val Pro Ile Leu Leu Ser

525

530

535

ctg gtc aag atc ttc ctg gag acc cgc aag tcc tgg aga aag cct gag 1684

Leu Val Lys Ile Phe Leu Glu Thr Arg Lys Ser Trp Arg Lys Pro Glu

540

545

550

aag aca gac tgagcagggc agcacctcca taggaagcct tcctttctgg 1733

Lys Thr Asp

555

ccaaggtggg cgggtgtaga ttgtgaggca cgtacatggg gcctgccgga atgacttaaa 1793

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tcaaaaggca catcatccgg gtctccttat cttgtttgat aaggctgctg cctgtctccc 1973

tctgtggcaa ggactgtttg ttcttttgcc ccatttctca acatagcaca cttgtgcact 2033

gagaggaggg agcattatgg gaaagtcctt gccttcaca cctctctcta gtccctgtgg 2093

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2518

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<212> PRT

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30

Pro Leu Trp Trp Lys Thr Thr Glu Thr Tyr Arg Ala Ser Leu Pro Tyr

35

40

45

Ser Gln Ile Ser Gly Leu Asn Ala Leu Gln Leu Arg Leu Met Val Pro

50

55

60

Val Thr Val Val Phe Thr Arg Glu Ser Val Pro Leu Asp Asp Gln Glu

65

70

75

80

Lys Leu Pro Phe Thr Val Val His Glu Arg Glu Ile Pro Leu Lys Tyr

85

90

95

Lys Met Lys Ile Lys Cys Arg Phe Gln Lys Ala Tyr Arg Arg Ala Leu

100

105

110

Asp His Glu Glu Glu Ala Leu Ser Ser Gly Ser Val Gln Glu Ala Glu

115

120

125

Ala Met Leu Asp Glu Pro Gln Glu Gln Ala Glu Gly Ser Leu Thr Val

130

135

140

Tyr Val Ile Ser Glu His Ser Ser Leu Leu Pro Gln Asp Met Met Ser

145

150

155

160

Tyr Ile Gly Pro Lys Arg Thr Ala Val Val Arg Gly Ile Met His Arg

165

170

175

Glu Ala Phe Asn Ile Ile Gly Arg Arg Ile Val Gln Val Ala Gln Ala

180

185

190

Met Ser Leu Thr Glu Asp Val Leu Ala Ala Ala Leu Ala Asp His Leu

195

200

205

Pro Glu Asp Lys Trp Ser Ala Glu Lys Arg Arg Pro Leu Lys Ser Ser

210

215

220

Leu Gly Tyr Glu Ile Thr Phe Ser Leu Leu Asn Pro Asp Pro Lys Ser

225

230

235

240

His Asp Val Tyr Trp Asp Ile Glu Gly Ala Val Arg Arg Tyr Val Gln

245

250

255

Pro Ser Leu Asn Ala Leu Gly Ala Ala Gly Asn Phe Ser Val Asp Ser

260

265

270

Gln Ile Leu Tyr Tyr Ala Met Leu Gly Val Asn Pro Arg Phe Asp Ser
275 280 285

Ala Ser Ser Ser Tyr Tyr Leu Asp Met His Ser Leu Pro His Val Ile
290 295 300

Asn Pro Val Glu Ser Arg Leu Gly Ser Ser Ala Ala Ser Leu Tyr Pro
305 310 315 320

Val Leu Asn Phe Leu Leu Tyr Val Pro Glu Leu Ala His Ser Pro Leu
325 330 335

Tyr Ile Gln Asp Lys Asp Gly Ala Pro Val Ala Thr Asn Ala Phe His
340 345 350

Ser Pro Arg Trp Gly Gly Ile Met Val Tyr Asn Val Asp Ser Lys Thr
355 360 365

Tyr Asn Ala Ser Val Leu Pro Val Arg Val Glu Val Asp Met Val Arg
370 375 380

Val Met Glu Val Phe Leu Ala Gln Leu Arg Leu Leu Phe Gly Ile Ala
385 390 395 400

Gln Pro Gln Leu Pro Pro Lys Cys Leu Leu Ser Gly Pro Thr Ser Glu
405 410 415

Gly Leu Met Thr Trp Glu Leu Asp Arg Leu Leu Trp Ala Arg Ser Val
420 425 430

Glu Asn Leu Ala Thr Ala Thr Thr Thr Leu Thr Ser Leu Ala Gln Leu

435

440

445

Leu Gly Lys Ile Ser Asn Ile Val Ile Lys Asp Asp Val Ala Ser Glu

450

455

460

Val Tyr Lys Ala Val Ala Ala Val Gln Lys Ser Ala Glu Glu Leu Ala

465

470

475

480

Ser Gly His Leu Ala Ser Ala Phe Val Ala Ser Gln Glu Ala Val Thr

485

490

495

Ser Ser Glu Leu Ala Phe Phe Asp Pro Ser Leu Leu His Leu Leu Tyr

500

505

510

Phe Pro Asp Tyr Gln Lys Phe Ala Ile Tyr Ile Pro Leu Phe Leu Pro

515

520

525

Met Ala Val Pro Ile Leu Leu Ser Leu Val Lys Ile Phe Leu Glu Thr

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Arg Lys Ser Trp Arg Lys Pro Glu Lys Thr Asp

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gaggacctgg tgcattgctg cctcctaata ccatagtcca gaggaggcat ccctaggact 180

gcgggcaagg gagccgggca agcccagggc agccttgaac cgtccccctgg cctgccctcc 240

ccggtggggg ccagg atg ctg aag aag cag tct gca ggg ctt gtg ctg tgg 291

Met Leu Lys Lys Gln Ser Ala Gly Leu Val Leu Trp

1

5

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ggc gct atc ctc ttt gtg gcc tgg aat gcc ctg ctg ctc ctc ttc ttc 339

Gly Ala Ile Leu Phe Val Ala Trp Asn Ala Leu Leu Leu Leu Phe Phe

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tgg acg cgc cca gca cct ggc agg cca ccc tca gtc agc gct ctc gat 387

Trp Thr Arg Pro Ala Pro Gly Arg Pro Pro Ser Val Ser Ala Leu Asp

30

35

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ggc gac ccc gcc agc ctc acc cag gtc ttc cgg cag ttt cgc ttc ccc 435

Gly Asp Pro Ala Ser Leu Thr Gln Val Phe Arg Gln Phe Arg Phe Pro

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gcg gcc gtg gtg gtg gag gat gac ctg gag gtg gcc ccg gac ttc ttc 483			
Ala Ala Val Val Val Glu Asp Asp Leu Glu Val Ala Pro Asp Phe Phe			
65	70	75	
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gag tac ttt cag gcc acc tat ccg ctg ctg aag gcc gac ccc tcc ctg 531			
Glu Tyr Phe Gln Ala Thr Tyr Pro Leu Leu Lys Ala Asp Pro Ser Leu			
80	85	90	
tgg tgc gtc tgc gcc tgg aat gac aac ggc aag gag cag atg gtg gac 579			
Trp Cys Val Ser Ala Trp Asn Asp Asn Gly Lys Glu Gln Met Val Asp			
95	100	105	
gcc agc agg cct gag ctg ctc tac cgc acc gac ttt ttc cct ggc ctg 627			
Ala Ser Arg Pro Glu Leu Leu Tyr Arg Thr Asp Phe Phe Pro Gly Leu			
110	115	120	
ggc tgg ctg ctg ttg gcc gag ctc tgg gct gag ctg gag ccc aag tgg 675			
Gly Trp Leu Leu Leu Ala Glu Leu Trp Ala Glu Leu Glu Pro Lys Trp			
125	130	135	140
cca aag gcc ttc tgg gac gac tgg atg cgg cgg ccg gag cag cgg cag 723			
Pro Lys Ala Phe Trp Asp Asp Trp Met Arg Arg Pro Glu Gln Arg Gln			
145	150	155	
ggg cgg gcc tgc ata cgc cct gag atc tca aga acg atg acc ttt ggc 771			
Gly Arg Ala Cys Ile Arg Pro Glu Ile Ser Arg Thr Met Thr Phe Gly			
160	165	170	

cgc aag ggt gtg agc cac ggg cag ttc ttt gac cag cac ctc aag ttt 819

Arg Lys Gly Val Ser His Gly Gln Phe Phe Asp Gln His Leu Lys Phe

175

180

185

atc aag ctg aac cag cag ttt gtg cac ttc acc cag ctg gac ctg tct 867

Ile Lys Leu Asn Gln Gln Phe Val His Phe Thr Gln Leu Asp Leu Ser

190

195

200

tac ctg cag cgg gag gcc tat gac cga gat ttc ctc gcc cgc gtc tac 915

Tyr Leu Gln Arg Glu Ala Tyr Asp Arg Asp Phe Leu Ala Arg Val Tyr

205

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215

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ggt gct ccc cag ctg cag gtg gag aaa gtg agg acc aat gac cgg aag 963

Gly Ala Pro Gln Leu Gln Val Glu Lys Val Arg Thr Asn Asp Arg Lys

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230

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gag ttg ggg gag gtt cgg gtg cag tat acg ggc agg gac agc ttc aag 1011

Glu Leu Gly Glu Val Arg Val Gln Tyr Thr Gly Arg Asp Ser Phe Lys

240

245

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gct ttc gcc aag gct ctg ggt gtc atg gat gac ctt aag tcg ggg gtt 1059

Ala Phe Ala Lys Ala Leu Gly Val Met Asp Asp Leu Lys Ser Gly Val

255

260

265

ccg aga gct ggc tac cgg ggt att gtc acc ttc cag ttc cgg ggc cgc 1107

Pro Arg Ala Gly Tyr Arg Gly Ile Val Thr Phe Gln Phe Arg Gly Arg

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275

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cgt gtc cac ctg gcg ccc cca ccg acg tgg gag ggc tat gat cct agc 1155
 Arg Val His Leu Ala Pro Pro Pro Thr Trp Glu Gly Tyr Asp Pro Ser
 285 290 295 300

tgg aat tagcacctgc ctgtccttcc tgggcccctc ctgcccacat catgagctga 1211
 Trp Asn

ggtgggacca cagtccccag gctgcatcgg cctgcctgtg tttccctctt aggtgcattt 1271

atctttttga tttttccgag tggcatttaa gtgcacaaat gataacaaga ggattattct 1331

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ataaaggctg aattgtctg 2250

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<211> 302

<212> PRT

<213> Homo sapiens

<400> 126

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Phe Val Ala Trp Asn Ala Leu Leu Leu Phe Phe Trp Thr Arg Pro

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Ala Pro Gly Arg Pro Pro Ser Val Ser Ala Leu Asp Gly Asp Pro Ala

35 40 45

Ser Leu Thr Gln Val Phe Arg Gln Phe Arg Phe Pro Ala Ala Val Val
50 55 60

Val Glu Asp Asp Leu Glu Val Ala Pro Asp Phe Phe Glu Tyr Phe Gln
65 70 75 80

Ala Thr Tyr Pro Leu Leu Lys Ala Asp Pro Ser Leu Trp Cys Val Ser
85 90 95

Ala Trp Asn Asp Asn Gly Lys Glu Gln Met Val Asp Ala Ser Arg Pro
100 105 110

Glu Leu Leu Tyr Arg Thr Asp Phe Phe Pro Gly Leu Gly Trp Leu Leu
115 120 125

Leu Ala Glu Leu Trp Ala Glu Leu Glu Pro Lys Trp Pro Lys Ala Phe
130 135 140

Trp Asp Asp Trp Met Arg Arg Pro Glu Gln Arg Gln Gly Arg Ala Cys
145 150 155 160

Ile Arg Pro Glu Ile Ser Arg Thr Met Thr Phe Gly Arg Lys Gly Val
165 170 175

Ser His Gly Gln Phe Phe Asp Gln His Leu Lys Phe Ile Lys Leu Asn
180 185 190

Gln Gln Phe Val His Phe Thr Gln Leu Asp Leu Ser Tyr Leu Gln Arg

195

200

205

Glu Ala Tyr Asp Arg Asp Phe Leu Ala Arg Val Tyr Gly Ala Pro Gln

210

215

220

Leu Gln Val Glu Lys Val Arg Thr Asn Asp Arg Lys Glu Leu Gly Glu

225

230

235

240

Val Arg Val Gln Tyr Thr Gly Arg Asp Ser Phe Lys Ala Phe Ala Lys

245

250

255

Ala Leu Gly Val Met Asp Asp Leu Lys Ser Gly Val Pro Arg Ala Gly

260

265

270

Tyr Arg Gly Ile Val Thr Phe Gln Phe Arg Gly Arg Arg Val His Leu

275

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Ala Pro Pro Pro Thr Trp Glu Gly Tyr Asp Pro Ser Trp Asn

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<210> 127

<211> 1666

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (199)..(1272)

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cgggtgggct ggcgagccga cgcggcggcg gaggaggctg tgaggagtgt gtggaacagg 180

accgaggaca gaggaacc atg gct ccg cag aac ctg agc acc ttt tgc ctg 231

Met Ala Pro Gln Asn Leu Ser Thr Phe Cys Leu

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Leu Leu Leu Tyr Leu Ile Gly Ala Val Ile Ala Gly Arg Asp Phe Tyr

15 20 25

aag atc ttg ggg gtg cct cga agt gcc tct ata aag gat att aaa aag 327

Lys Ile Leu Gly Val Pro Arg Ser Ala Ser Ile Lys Asp Ile Lys Lys

30 35 40

gcc tat agg aaa cta gcc ctg cag ctt cat ccc gac cgg aac cct gat 375

Ala Tyr Arg Lys Leu Ala Leu Gln Leu His Pro Asp Arg Asn Pro Asp

45 50 55

gat cca caa gcc cag gag aaa ttc cag gat ctg ggt gct gct tat gag 423

Asp Pro Gln Ala Gln Glu Lys Phe Gln Asp Leu Gly Ala Ala Tyr Glu

60 65 70 75

gtt ctg tca gat agt gag aaa cgg aaa cag tac gat act tat ggt gaa 471

Val Leu Ser Asp Ser Glu Lys Arg Lys Gln Tyr Asp Thr Tyr Gly Glu

80

85

90

gaa gga tta aaa gat ggt cat cag agc tcc cat gga gac att ttt tca 519

Glu Gly Leu Lys Asp Gly His Gln Ser Ser His Gly Asp Ile Phe Ser

95

100

105

cac ttc ttt ggg gat ttt ggt ttc atg ttt gga gga acc cct cgt cag 567

His Phe Phe Gly Asp Phe Gly Phe Met Phe Gly Gly Thr Pro Arg Gln

110

115

120

caa gac aga aat att cca aga gga agt gat att att gta gat cta gaa 615

Gln Asp Arg Asn Ile Pro Arg Gly Ser Asp Ile Ile Val Asp Leu Glu

125

130

135

gtc act ttg gaa gaa gta tat gca gga aat ttt gtg gaa gta gtt aga 663

Val Thr Leu Glu Glu Val Tyr Ala Gly Asn Phe Val Glu Val Val Arg

140

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aac aaa cct gtg gca agg cag gct cct ggc aaa cgg aag tgc aat tgt 711

Asn Lys Pro Val Ala Arg Gln Ala Pro Gly Lys Arg Lys Cys Asn Cys

160

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cgg caa gag atg cgg acc acc cag ctg ggc cct ggg cgc ttc caa atg 759

Arg Gln Glu Met Arg Thr Thr Gln Leu Gly Pro Gly Arg Phe Gln Met

175

180

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acc cag gag gtg gtc tgc gac gaa tgc cct aat gtc aaa cta gtg aat 807

Thr Gln Glu Val Val Cys Asp Glu Cys Pro Asn Val Lys Leu Val Asn

190

195

200

gaa gaa cga acg ctg gaa gta gaa ata gag cct ggg gtg aga gac ggc 855

Glu Glu Arg Thr Leu Glu Val Glu Ile Glu Pro Gly Val Arg Asp Gly

205

210

215

atg gag tac ccc ttt att gga gaa ggt gag cct cac gtg gat ggg gag 903

Met Glu Tyr Pro Phe Ile Gly Glu Gly Glu Pro His Val Asp Gly Glu

220

225

230

235

cct gga gat tta cgg ttc cga atc aaa gtt gtc aag cac cca ata ttt 951

Pro Gly Asp Leu Arg Phe Arg Ile Lys Val Val Lys His Pro Ile Phe

240

245

250

gaa agg aga gga gat gat ttg tac aca aat gtg aca att tca tta gtt 999

Glu Arg Arg Gly Asp Asp Leu Tyr Thr Asn Val Thr Ile Ser Leu Val

255

260

265

gag tca ctg gtt ggc ttt gag atg gat att act cac ttg gat ggt cac 1047

Glu Ser Leu Val Gly Phe Glu Met Asp Ile Thr His Leu Asp Gly His

270

275

280

aag gta cat att tcc cgg gat aag atc acc agg cca gga gcg aag cta 1095

Lys Val His Ile Ser Arg Asp Lys Ile Thr Arg Pro Gly Ala Lys Leu

285

290

295

tgg aag aaa ggg gaa ggg ctc ccc aac ttt gac aac aac aat atc aag 1143

Trp Lys Lys Gly Glu Gly Leu Pro Asn Phe Asp Asn Asn Asn Ile Lys

300

305

310

315

ggc tct ttg ata atc act ttt gat gtg gat ttt cca aaa gaa cag tta 1191

Gly Ser Leu Ile Ile Thr Phe Asp Val Asp Phe Pro Lys Glu Gln Leu

320

325

330

aca gag gaa gcg aga gaa ggt atc aaa cag cta ctg aaa caa ggg tca 1239

Thr Glu Glu Ala Arg Glu Gly Ile Lys Gln Leu Leu Lys Gln Gly Ser

335

340

345

gtg cag aag gta tac aat gga ctg caa gga tat tgagagtga taaaattgga 1292

Val Gln Lys Val Tyr Asn Gly Leu Gln Gly Tyr

350

355

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1666

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<212> PRT

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<400> 128

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Ile Gly Ala Val Ile Ala Gly Arg Asp Phe Tyr Lys Ile Leu Gly Val

20

25

30

Pro Arg Ser Ala Ser Ile Lys Asp Ile Lys Lys Ala Tyr Arg Lys Leu

35

40

45

Ala Leu Gln Leu His Pro Asp Arg Asn Pro Asp Asp Pro Gln Ala Gln

50

55

60

Glu Lys Phe Gln Asp Leu Gly Ala Ala Tyr Glu Val Leu Ser Asp Ser

65

70

75

80

Glu Lys Arg Lys Gln Tyr Asp Thr Tyr Gly Glu Glu Gly Leu Lys Asp

85

90

95

Gly His Gln Ser Ser His Gly Asp Ile Phe Ser His Phe Phe Gly Asp

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105

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Phe Gly Phe Met Phe Gly Gly Thr Pro Arg Gln Gln Asp Arg Asn Ile

115

120

125

Pro Arg Gly Ser Asp Ile Ile Val Asp Leu Glu Val Thr Leu Glu Glu
130 135 140

Val Tyr Ala Gly Asn Phe Val Glu Val Val Arg Asn Lys Pro Val Ala
145 150 155 160

Arg Gln Ala Pro Gly Lys Arg Lys Cys Asn Cys Arg Gln Glu Met Arg
165 170 175

Thr Thr Gln Leu Gly Pro Gly Arg Phe Gln Met Thr Gln Glu Val Val
180 185 190

Cys Asp Glu Cys Pro Asn Val Lys Leu Val Asn Glu Glu Arg Thr Leu
195 200 205

Glu Val Glu Ile Glu Pro Gly Val Arg Asp Gly Met Glu Tyr Pro Phe
210 215 220

Ile Gly Glu Gly Glu Pro His Val Asp Gly Glu Pro Gly Asp Leu Arg
225 230 235 240

Phe Arg Ile Lys Val Val Lys His Pro Ile Phe Glu Arg Arg Gly Asp
245 250 255

Asp Leu Tyr Thr Asn Val Thr Ile Ser Leu Val Glu Ser Leu Val Gly
260 265 270

Phe Glu Met Asp Ile Thr His Leu Asp Gly His Lys Val His Ile Ser
275 280 285

Arg Asp Lys Ile Thr Arg Pro Gly Ala Lys Leu Trp Lys Lys Gly Glu

290

295

300

Gly Leu Pro Asn Phe Asp Asn Asn Asn Ile Lys Gly Ser Leu Ile Ile

305

310

315

320

Thr Phe Asp Val Asp Phe Pro Lys Glu Gln Leu Thr Glu Glu Ala Arg

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340

345

350

Asn Gly Leu Gln Gly Tyr

355

<210> 129

<211> 1686

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (121)..(1548)

<400> 129

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atg gtt ggt gcc atg tgg aag gtg att gtt tcg ctg gtc ctg ttg atg 168

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met

1

5

10

15

cct ggc ccc tgt gat ggg ctg ttt cgc tcc cta tac aga agt gtt tcc 216

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser

20

25

30

atg cca cct aag gga gac tca gga cag cca tta ttt ctc acc cct tac 264

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr

35

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45

att gaa gct ggg aag atc caa aaa gga aga gaa ttg agt ttg gtc ggc 312

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly

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cct ttc cca gga ctg aac atg aag agt tat gcc ggc ttc ctc acc gtg 360

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

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70

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80

aat aag act tac aac agc aac ctc ttc ttc tgg ttc ttc cca gct cag 408

Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln

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90

95

ata cag cca gaa gat gcc cca gta gtt ctc tgg cta cag ggt ggg ccg 456

Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro

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105

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gga ggt tca tcc atg ttt gga ctc ttt gtg gaa cat ggg cct tat gtt 504

Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val

115

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gtc aca agt aac atg acc ttg cgt gac aga gac ttc ccc tgg acc aca 552

Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr

130

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acg ctc tcc atg ctt tac att gac aat cca gtg ggc aca ggc ttc agt 600

Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser

145

150

155

160

ttt act gat gat acc cac gga tat gca gtc aat gag gac gat gta gca 648

Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala

165

170

175

cgg gat tta tac agt gca cta att cag ttt ttc cag ata ttt cct gaa 696

Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu

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tat aaa aat aat gac ttt tat gtc act ggg gag tct tat gca ggg aaa 744

Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys

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tat gtg cca gcc att gca cac ctc atc cat tcc ctc aac cct gtg aga 792

Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg

210

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gag gtg aag atc aac ctg aac gga att gct att gga gat gga tat tct 840
 Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser
 225 230 235 240

gat ccc gaa tca att ata ggg ggc tat gca gaa ttc ctg tac caa att 888
 Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile

245

250

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ggc ttg ttg gat gag aag caa aaa aag tac ttc cag aag cag tgc cat 936
 Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His
 260 265 270

gaa tgc ata gaa cac atc agg aag cag aac tgg ttt gag gcc ctt gaa 984
 Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Leu Glu
 275 280 285

ata ctg gat aaa cta cta gat ggc gac tta aca agt gat cct tct tac 1032
 Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr
 290 295 300

ttc cag aat gtt aca gga tgt agt aat tac tat aac ttt ttg cgg tgc 1080
 Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys
 305 310 315 320

acg gaa cct gag gat cag ctt tac tat gtg aaa ttt ttg tca ctc cca 1128
 Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro
 325 330 335

gag gtg aga caa gcc atc cac gtg ggg aat cag act ttt aat gat gga 1176

Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly

340

345

350

act ata gtt gaa aag tac ttg cga gaa gat aca gta cag tca gtt aag 1224

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys

355

360

365

cca tgg tta act gaa atc atg aat aat tat aag gtt ctg atc tac aat 1272

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn

370

375

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ggc caa ctg gac atc atc gtg gca gct gcc ctg aca gag cgc tcc ttg 1320

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu

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390

395

400

atg ggc atg gac tgg aaa gga tcc cag gaa tac aag aag gca gaa aaa 1368

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys

405

410

415

aaa gtt tgg aag atc ttt aaa tct gac agt gaa gtg gct ggt tac atc 1416

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile

420

425

430

cgg caa gtg ggt gac ttc cat cag gta att att cga ggt gga gga cat 1464

Arg Gln Val Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His

435

440

445

att tta ccc tat gac cag cct ctg aga gct ttt gac atg att aat cga 1512

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg

450

455

460

ttc att tat gga aaa gga tgg gat cct tat gtt gga taaactacct 1558

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly

465

470

475

tcctaaaaga gaacatcaga gggttttcatt gctgaaaaga aaatcgtaaa aacagaaaaat 1618

gtcataggaa taaaaaaatt atcttttcat atctgcaaga tttttttcat caataaaaaat 1678

tatccttg 1686

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<211> 476

<212> PRT

<213> Homo sapiens

<400> 130

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Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser

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30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr

35

40

45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly

50

55

60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65

70

75

80

Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln

85

90

95

Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro

100

105

110

Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val

115

120

125

Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr

130

135

140

Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser

145

150

155

160

Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala

165

170

175

Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu

180

185

190

Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys

195

200

205



Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg
210 215 220

Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser
225 230 235 240

Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile
245 250 255

Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His
260 265 270

Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Leu Glu
275 280 285

Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr
290 295 300

Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys
305 310 315 320

Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro
325 330 335

Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly
340 345 350

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys
355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn

370

375

380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu

385

390

395

400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys

405

410

415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile

420

425

430

Arg Gln Val Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His

435

440

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Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly

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<210> 131

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<212> DNA

<213> Homo sapiens

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<400> 131

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atg aag tat ctc cgg cac cgg cgg ccc aat gcc acc ctc att ctg gcc 168

Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala

1

5

10

15

atc ggc gct ttc acc ctc ctc ctc ttc agt ctg cta gtg tca cca ccc 216

Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro

20

25

30

acc tgc aag gtc cag gag cag cca ccg gcg atc ccc gag gcc ctg gcc 264

Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala

35

40

45

tgg ccc act cca ccc acc cgc cca gcc ccg gcc ccg tgc cat gcc aac 312

Trp Pro Thr Pro Pro Thr Arg Pro Ala Pro Ala Pro Cys His Ala Asn

50

55

60

acc tct atg gtc acc cac ccg gac ttc gcc acg cag ccg cag cac gtt 360

Thr Ser Met Val Thr His Pro Asp Phe Ala Thr Gln Pro Gln His Val

65

70

75

80

cag aac ttc ctc ctg tac aga cac tgc cgc cac ctc ttc gtg ggg caa 408

Gln Asn Phe Leu Leu Tyr Arg His Cys Arg His Leu Phe Val Gly Gln

85

90

95

ctg atc caa aac gtg ggc ccc atc cgg gct ttt tgg agc aag tac tat 456

Leu Ile Gln Asn Val Gly Pro Ile Arg Ala Phe Trp Ser Lys Tyr Tyr

100

105

110

gtg cca gag gtg gtg act cag aat gag cgg tac cca ccc tat tgt ggg 504

Val Pro Glu Val Val Thr Gln Asn Glu Arg Tyr Pro Pro Tyr Cys Gly

115

120

125

ggg ggt ggc ttc ttg ctg tcc cgc ttc acg gcc gct gcc ctg cgc cgt 552

Gly Gly Gly Phe Leu Leu Ser Arg Phe Thr Ala Ala Ala Leu Arg Arg

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gct gcc cat gtc ttg gac atc ttc ccc att gat gat gtc ttc ctg ggt 600

Ala Ala His Val Leu Asp Ile Phe Pro Ile Asp Asp Val Phe Leu Gly

145

150

155

160

atg tgt ctg gag ctt gag gga ctg aag cct gcc tcc cac agc ggc atc 648

Met Cys Leu Glu Leu Glu Gly Leu Lys Pro Ala Ser His Ser Gly Ile

165

170

175

cgc acg tct ggc gtg cgg gct cca tcg caa cgc ctg tcc tcc ttt gac 696

Arg Thr Ser Gly Val Arg Ala Pro Ser Gln Arg Leu Ser Ser Phe Asp

180

185

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ccc tgc ttc tac cga gac ctg ctg ctg gtg cac cgc ttc cta cct tat 744

Pro Cys Phe Tyr Arg Asp Leu Leu Leu Val His Arg Phe Leu Pro Tyr

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gag atg ctg ctc atg tgg gat gcg ctg aac cag ccc aac ctc acc tgc 792			
Glu Met Leu Leu Met Trp Asp Ala Leu Asn Gln Pro Asn Leu Thr Cys			
210	215	220	

ggc aat cag aca cag atc tac cga gtc agc atc agg gtc ccc agc ctc 840			
Gly Asn Gln Thr Gln Ile Tyr Arg Val Ser Ile Arg Val Pro Ser Leu			
225	230	235	240

tgg gct cct gtt tcc ata gga agg ggc gac acc ttc ctc cca gga agc 888			
Trp Ala Pro Val Ser Ile Gly Arg Gly Asp Thr Phe Leu Pro Gly Ser			
245	250	255	

tgagaccttt gtggtctgag cataagggag tgccagggaa ggtttgaggt ttgatgagtg 948

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<213> Homo sapiens.

<400> 132

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Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro

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Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala

35 40 45

Trp Pro Thr Pro Pro Thr Arg Pro Ala Pro Ala Pro Cys His Ala Asn

50 55 60

Thr Ser Met Val Thr His Pro Asp Phe Ala Thr Gln Pro Gln His Val

65 70 75 80

Gln Asn Phe Leu Leu Tyr Arg His Cys Arg His Leu Phe Val Gly Gln

85 90 95

Leu Ile Gln Asn Val Gly Pro Ile Arg Ala Phe Trp Ser Lys Tyr Tyr

100 105 110

Val Pro Glu Val Val Thr Gln Asn Glu Arg Tyr Pro Pro Tyr Cys Gly

115 120 125

Gly Gly Gly Phe Leu Leu Ser Arg Phe Thr Ala Ala Ala Leu Arg Arg

130 135 140

Ala Ala His Val Leu Asp Ile Phe Pro Ile Asp Asp Val Phe Leu Gly

145 150 155 160

Met Cys Leu Glu Leu Glu Gly Leu Lys Pro Ala Ser His Ser Gly Ile

165 170 175

Arg Thr Ser Gly Val Arg Ala Pro Ser Gln Arg Leu Ser Ser Phe Asp

180 185 190

Pro Cys Phe Tyr Arg Asp Leu Leu Leu Val His Arg Phe Leu Pro Tyr

195 200 205

Glu Met Leu Leu Met Trp Asp Ala Leu Asn Gln Pro Asn Leu Thr Cys

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225 230 235 240

Trp Ala Pro Val Ser Ile Gly Arg Gly Asp Thr Phe Leu Pro Gly Ser

245 250 255

<210> 133

<211> 1906

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (48)..(353)

<400> 133

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Met Ser Leu

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Leu Ser Leu Pro Trp Leu Gly Leu Arg Pro Val Ala Met Ser Pro Trp

5

10

15

cta ctc ctg ctg ctg gtt gtg ggc tcc tgg cta ctc gcc cgc atc ctg 152

Leu Leu Leu Leu Leu Val Val Gly Ser Trp Leu Leu Ala Arg Ile Leu

20

25

30

35

gct tgg acc tat gcc ttc tat aac aac tgc cgc cgg ctc cag tgt ttc 200

Ala Trp Thr Tyr Ala Phe Tyr Asn Asn Cys Arg Arg Leu Gln Cys Phe

40

45

50

cca cag ccc cca aaa cgg aac tgg ttt tgg ggt cac ctg ggc ctg atc 248

Pro Gln Pro Pro Lys Arg Asn Trp Phe Trp Gly His Leu Gly Leu Ile

55

60

65

act cct aca gag gag ggc ttg aag gac tcg acc cag atg tcg gcc acc 296

Thr Pro Thr Glu Glu Gly Leu Lys Asp Ser Thr Gln Met Ser Ala Thr

70

75

80

tat tcc cag ggc ttt acg ctg cca ttg cac cca agg ata atc tct tca 344

Tyr Ser Gln Gly Phe Thr Leu Pro Leu His Pro Arg Ile Ile Ser Ser

85

90

95

tca ggt tcc tgaagccctg gctgggtgag tacctgcagg tgaaaggggt 393

Ser Gly Ser

100

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ccctactagg agaagggata ctgctgagtg gcggtgacaa gtggagccgc caccgtcgga 513

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gtgctgtcac etc

1906

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<211> 102

<212> PRT

<213> Homo sapiens

<400> 134

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Ser Pro Trp Leu Leu Leu Leu Val Val Gly Ser Trp Leu Leu Ala

20 25 30

Arg Ile Leu Ala Trp Thr Tyr Ala Phe Tyr Asn Asn Cys Arg Arg Leu

35 40 45

Gln Cys Phe Pro Gln Pro Pro Lys Arg Asn Trp Phe Trp Gly His Leu

50 55 60

Gly Leu Ile Thr Pro Thr Glu Glu Gly Leu Lys Asp Ser Thr Gln Met

65 70 75 80

Ser Ala Thr Tyr Ser Gln Gly Phe Thr Leu Pro Leu His Pro Arg Ile

85 90 95

Ile Ser Ser Ser Gly Ser

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<210> 135

<211> 1773

<212> DNA

<213> Homo sapiens

<220>

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<222> (1)..(654)

<400> 135

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tct ccg ggc gtg gaa cgg gtc tgt ttc cgg gct cga atc cag ccc tgg 96

Ser Pro Gly Val Glu Arg Val Cys Phe Arg Ala Arg Ile Gln Pro Trp

20 25 30

cac ggt ggc ctg ctc caa ccg cta cct tgc tct ttc gag atg ggg ctg 144

His Gly Gly Leu Leu Gln Pro Leu Pro Cys Ser Phe Glu Met Gly Leu

35 40 45

cca cgc cgc cgg ttc agc tcc gag gcc gca gaa tct ggt agc cca gag 192

Pro Arg Arg Arg Phe Ser Ser Glu Ala Ala Glu Ser Gly Ser Pro Glu

50 55 60

acc aag aaa cct aca ttt atg gat gag gaa gtt caa agc ata ctc acg 240

Thr Lys Lys Pro Thr Phe Met Asp Glu Glu Val Gln Ser Ile Leu Thr

65 70 75 80

aaa atg aca ggc ttg aac ttg cag aag act ttt aag cca gct ata caa 288

Lys Met Thr Gly Leu Asn Leu Gln Lys Thr Phe Lys Pro Ala Ile Gln

85

90

95

gaa ctg aag cca cca acc tat aag cta atg act cag gca cag ttg gaa 336

Glu Leu Lys Pro Pro Thr Tyr Lys Leu Met Thr Gln Ala Gln Leu Glu

100

105

110

gag gct aca aga cag gca gtt gag gca gct aaa gta cga tta aaa atg 384

Glu Ala Thr Arg Gln Ala Val Glu Ala Ala Lys Val Arg Leu Lys Met

115

120

125

cca cca gtt ctg gaa gag cga gta cca ata aat gat gtg tta gct gaa 432

Pro Pro Val Leu Glu Glu Arg Val Pro Ile Asn Asp Val Leu Ala Glu

130

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gat aag att ttg gaa gga aca gaa aca acc aaa tat gtg ttt act gat 480

Asp Lys Ile Leu Glu Gly Thr Glu Thr Thr Lys Tyr Val Phe Thr Asp

145

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155

160

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Ile Ser Tyr Ser Ile Pro His Arg Glu Arg Phe Ile Val Val Arg Glu

165

170

175

cca agt ggc aca cta cgc aaa gcc tct tgg gaa gaa cgg gac cga atg 576

Pro Ser Gly Thr Leu Arg Lys Ala Ser Trp Glu Glu Arg Asp Arg Met

180

185

190

ata caa gtt tat ttc cca aaa gaa ggt cgt aaa att ttg aca cca ata 624

Ile Gln Val Tyr Phe Pro Lys Glu Gly Arg Lys Ile Leu Thr Pro Ile

195

200

205

att ttc aag gaa gaa aat ctt agg gta agg tgacttaggt tttatgtttt 674

Ile Phe Lys Glu Glu Asn Leu Arg Val Arg

210

215

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ccaggctgaa gtgcagtggc gggatctcag ctcactgcaa cctccacctt ctggtttcaa 854

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aagacctatg aagatataga taaacgtggg aaatatgacc ttttacgttc aacaagatac 1454

tttggtggaa tgggtgtggt ttttgtaaata aataaaaaga ttgatgggtt gctgattgac 1514

cagattcaga gagatttaata cgatgatgca accaacttgg tccagctgta tcacgtgctc 1574

catccagatg gccagtcggc tcaaggggcc aaggatcagg ctgctgaggg aataaattta 1634

atcaaggctt ttgcaaaaac agaagcacag aaggagcct atatagaact aacactgcag 1694

acttatcaag aagcactcag tcgccattct gcagcttcct aaaaatatit taaaaataca 1754

tttatitttac taaatactg 1773

<210> 136

<211> 218

<212> PRT

<213> Homo sapiens

<400> 136

Met Ala Pro Leu Arg Thr Thr Val Leu Leu Trp Ser Leu Leu Arg Ser

1 5 10 15

Ser Pro Gly Val Glu Arg Val Cys Phe Arg Ala Arg Ile Gln Pro Trp

20 25 30

His Gly Gly Leu Leu Gln Pro Leu Pro Cys Ser Phe Glu Met Gly Leu

35

40

45

Pro Arg Arg Arg Phe Ser Ser Glu Ala Ala Glu Ser Gly Ser Pro Glu

50

55

60

Thr Lys Lys Pro Thr Phe Met Asp Glu Glu Val Gln Ser Ile Leu Thr

65

70

75

80

Lys Met Thr Gly Leu Asn Leu Gln Lys Thr Phe Lys Pro Ala Ile Gln

85

90

95

Glu Leu Lys Pro Pro Thr Tyr Lys Leu Met Thr Gln Ala Gln Leu Glu

100

105

110

Glu Ala Thr Arg Gln Ala Val Glu Ala Ala Lys Val Arg Leu Lys Met

115

120

125

Pro Pro Val Leu Glu Glu Arg Val Pro Ile Asn Asp Val Leu Ala Glu

130

135

140

Asp Lys Ile Leu Glu Gly Thr Glu Thr Thr Lys Tyr Val Phe Thr Asp

145

150

155

160

Ile Ser Tyr Ser Ile Pro His Arg Glu Arg Phe Ile Val Val Arg Glu

165

170

175

Pro Ser Gly Thr Leu Arg Lys Ala Ser Trp Glu Glu Arg Asp Arg Met

180

185

190

Ile Gln Val Tyr Phe Pro Lys Glu Gly Arg Lys Ile Leu Thr Pro Ile

195

200

205

Ile Phe Lys Glu Glu Asn Leu Arg Val Arg

210

215

<210> 137

<211> 2134

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74)..(991)

<400> 137

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Met Ala Leu Pro Pro Gly Pro Ala Ala Leu Arg His

1

5

10

aca ctg ctg ctc ctg cca gcc ctt ctg agc tca ggt tgg ggg gag ttg 157

Thr Leu Leu Leu Leu Pro Ala Leu Leu Ser Ser Gly Trp Gly Glu Leu

15

20

25

gag cca caa ata gat ggt cag acc tgg gct gag cgg gca ctt cgg gag 205

Glu Pro Gln Ile Asp Gly Gln Thr Trp Ala Glu Arg Ala Leu Arg Glu

30

35

40

aat gaa cgc cac gcc ttc acc tgc cgg gtg gca ggg ggg cct ggc acc 253

Asn Glu Arg His Ala Phe Thr Cys Arg Val Ala Gly Gly Pro Gly Thr

45

50

55

60

ccc aga ttg gcc tgg tat ctg gat gga cag ctg cag gag gcc agc acc 301

Pro Arg Leu Ala Trp Tyr Leu Asp Gly Gln Leu Gln Glu Ala Ser Thr

65

70

75

tca aga ctg ctg agc gtg gga ggg gag gcc ttc tct gga ggc acc agc 349

Ser Arg Leu Leu Ser Val Gly Gly Glu Ala Phe Ser Gly Gly Thr Ser

80

85

90

acc ttc act gtc act gcc cat cgg gcc cag cat gag ctc aac tgc tct 397

Thr Phe Thr Val Thr Ala His Arg Ala Gln His Glu Leu Asn Cys Ser

95

100

105

ctg cag gac ccc aga agt ggc cga tca gcc aac gcc tct gtc atc ctt 445

Leu Gln Asp Pro Arg Ser Gly Arg Ser Ala Asn Ala Ser Val Ile Leu

110

115

120

aat gtg caa ttc aag cca gag att gcc caa gtc ggc gcc aag tac cag 493

Asn Val Gln Phe Lys Pro Glu Ile Ala Gln Val Gly Ala Lys Tyr Gln

125

130

135

140

gaa gct cag ggc cca ggc ctc ctg gtt gtc ctg ttt gcc ctg gtg cgt 541

Glu Ala Gln Gly Pro Gly Leu Leu Val Val Leu Phe Ala Leu Val Arg

145

150

155

gcc aac ccg ccg gcc aat gtc acc tgg atc gac cag gat ggg cca gtg 589

Ala Asn Pro Pro Ala Asn Val Thr Trp Ile Asp Gln Asp Gly Pro Val

160

165

170

act gtc aac acc tct gac ttc ctg gtg ctg gat gcg cag aac tac ccc 637

Thr Val Asn Thr Ser Asp Phe Leu Val Leu Asp Ala Gln Asn Tyr Pro

175

180

185

tgg ctc acc aac cac acg gtg cag ctg cag ctc cgc agc ctg gca cac 685

Trp Leu Thr Asn His Thr Val Gln Leu Gln Leu Arg Ser Leu Ala His

190

195

200

aac ctc tcg gtg gtg gcc acc aat gac gtg ggt gtc acc agt gcg tcg 733

Asn Leu Ser Val Val Ala Thr Asn Asp Val Gly Val Thr Ser Ala Ser

205

210

215

220

ctt cca gcc cca ggc ccc tcc cgg cac cca tct ctg gta tca agt gac 781

Leu Pro Ala Pro Gly Pro Ser Arg His Pro Ser Leu Val Ser Ser Asp

225

230

235

tcc aac aac cta aaa ctc aac aac gtg cgc ctg cca cgg gag aac atg 829

Ser Asn Asn Leu Lys Leu Asn Asn Val Arg Leu Pro Arg Glu Asn Met

240

245

250

tcc ctc ccg tcc aac ctt cag ctc aat gac ctc act cca gat tcc agg 877

Ser Leu Pro Ser Asn Leu Gln Leu Asn Asp Leu Thr Pro Asp Ser Arg

255

260

265

gtg aaa cca gca gac cgg cag atg gct cag aac aac agc cgg cca gag 925

Val Lys Pro Ala Asp Arg Gln Met Ala Gln Asn Asn Ser Arg Pro Glu

270

275

280

ctt ctg gac ccg gag ccc ggc ggc ctc ctc acc agc cga gga aga aga 973

Leu Leu Asp Pro Glu Pro Gly Gly Leu Leu Thr Ser Arg Gly Arg Arg

285

290

295

300

aat cag gac aaa gac gca taacagaggg aagaccatgg gaagacacag 1021

Asn Gln Asp Lys Asp Ala

305

aagatggcca agaagagacc cctcagaaga aatcaatctt ggtggggcgt ggtggcttca 1081

cgcttgaat accagcactg tgggaggttg aggtgggcag atcgctgag cctaggagtt 1141

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cagagtacat atagtctgc aacttgctgc aatttgcttt tttcatttaa caacatatca 1861

ctgatatttc ttcataatag agcaaaataa ggccaaataa tattccattg catagtattt 1921

cactgaatgg atgtactgca acctagctat tcaatcccct aatcagacac cttcccctca 1981

actacagctt caaaatgctc tgaggaaaga gactgtttcc aaattctgtg tgtttacaat 2041

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caaaataagt aaataaagtc tatggtatgc tag 2134

<210> 138

<211> 306

<212> PRT

<213> Homo sapiens

<400> 138

Met Ala Leu Pro Pro Gly Pro Ala Ala Leu Arg His Thr Leu Leu Leu
1 5 10 15

Leu Pro Ala Leu Leu Ser Ser Gly Trp Gly Glu Leu Glu Pro Gln Ile
20 25 30

Asp Gly Gln Thr Trp Ala Glu Arg Ala Leu Arg Glu Asn Glu Arg His
35 40 45

Ala Phe Thr Cys Arg Val Ala Gly Gly Pro Gly Thr Pro Arg Leu Ala
50 55 60

Trp Tyr Leu Asp Gly Gln Leu Gln Glu Ala Ser Thr Ser Arg Leu Leu
65 70 75 80

Ser Val Gly Gly Glu Ala Phe Ser Gly Gly Thr Ser Thr Phe Thr Val
85 90 95

Thr Ala His Arg Ala Gln His Glu Leu Asn Cys Ser Leu Gln Asp Pro
100 105 110

Arg Ser Gly Arg Ser Ala Asn Ala Ser Val Ile Leu Asn Val Gln Phe
115 120 125

Lys Pro Glu Ile Ala Gln Val Gly Ala Lys Tyr Gln Glu Ala Gln Gly
130 135 140

Pro Gly Leu Leu Val Val Leu Phe Ala Leu Val Arg Ala Asn Pro Pro
145 150 155 160

Ala Asn Val Thr Trp Ile Asp Gln Asp Gly Pro Val Thr Val Asn Thr
165 170 175

Ser Asp Phe Leu Val Leu Asp Ala Gln Asn Tyr Pro Trp Leu Thr Asn
180 185 190

His Thr Val Gln Leu Gln Leu Arg Ser Leu Ala His Asn Leu Ser Val
195 200 205

Val Ala Thr Asn Asp Val Gly Val Thr Ser Ala Ser Leu Pro Ala Pro
210 215 220

Gly Pro Ser Arg His Pro Ser Leu Val Ser Ser Asp Ser Asn Asn Leu
225 230 235 240

Lys Leu Asn Asn Val Arg Leu Pro Arg Glu Asn Met Ser Leu Pro Ser
245 250 255

Asn Leu Gln Leu Asn Asp Leu Thr Pro Asp Ser Arg Val Lys Pro Ala
260 265 270

Asp Arg Gln Met Ala Gln Asn Asn Ser Arg Pro Glu Leu Leu Asp Pro
275 280 285

Glu Pro Gly Gly Leu Leu Thr Ser Arg Gly Arg Arg Asn Gln Asp Lys
290 295 300

Asp Ala

305

<210> 139

<211> 1828

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (83)..(487)

<400> 139

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gggcgacgtg cccgcttcca aa atg gcg gcg gcg gcg gta tct ggt gcg ctt 112

Met Ala Ala Ala Ala Val Ser Gly Ala Leu

1 5 10

ggc cgg gcg ggc tgg agg ctc ctg cag ctg cga tgc ctg ccc gtg gcc 160

Gly Arg Ala Gly Trp Arg Leu Leu Gln Leu Arg Cys Leu Pro Val Ala

15 20 25

cgt tgc cga caa gcc ctg gtg ccg cgt gcc ttc cat gct tca gct gtg 208

Arg Cys Arg Gln Ala Leu Val Pro Arg Ala Phe His Ala Ser Ala Val

30 35 40

ggg cta agg tct tca gat gag cag aag cag cag cct ccc aac tca ttt 256

Gly Leu Arg Ser Ser Asp Glu Gln Lys Gln Gln Pro Pro Asn Ser Phe

45

50

55

tct cag cag cat tct gag aca cag ggc gca gaa aaa cct gat cca gag 304

Ser Gln Gln His Ser Glu Thr Gln Gly Ala Glu Lys Pro Asp Pro Glu

60

65

70

tct tct cat tca ccc ccc agg tat aca gac cag ggc ggc gag gag gag 352

Ser Ser His Ser Pro Pro Arg Tyr Thr Asp Gln Gly Gly Glu Glu Glu

75

80

85

90

gag gac tat gaa agt gag gag cag ttg cag cac cgc atc ctg acg gca 400

Glu Asp Tyr Glu Ser Glu Glu Gln Leu Gln His Arg Ile Leu Thr Ala

95

100

105

gcc ctt gag ttt gtg ccc gcc cac ggg tgg aca gca gag gcg att gca 448

Ala Leu Glu Phe Val Pro Ala His Gly Trp Thr Ala Glu Ala Ile Ala

110

115

120

gaa gga gcc cag gtg tgt ata ggt gag ggt ggg gcc acc taaccaagat 497

Glu Gly Ala Gln Val Cys Ile Gly Glu Gly Gly Ala Thr

125

130

135

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ctttattttg tagttataaa gaacatacca tggagtgggt tcttgggagt tgtgtttctaa 677

aggcaatcta ttaggcaaga attgtctgtg atcaaaactc ccatgtttca ttgactctaa 737

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gactgctgct ttagattagg cagcaggctc atgttcaggc catgttgtag agaatcctcc 1037

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gggctgtata atggaggac ccgatcatta gatcagggtca cagctgcgag attgactggt 1637

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ggaattgggt cttgagagtt gtgttctaaa ggcaacctat tggcaagaat tgtctgtgat 1757

caaaactacc atatttcatt gactctaaga tgccattggt tgtaagaagc actattttta 1817

agtacatcag t 1828

<210> 140

<211> 135

<212> PRT

<213> Homo sapiens

<400> 140

Met Ala Ala Ala Val Ser Gly Ala Leu Gly Arg Ala Gly Trp Arg

1 5 10 15

Leu Leu Gln Leu Arg Cys Leu Pro Val Ala Arg Cys Arg Gln Ala Leu

20 25 30

Val Pro Arg Ala Phe His Ala Ser Ala Val Gly Leu Arg Ser Ser Asp

35 40 45

Glu Gln Lys Gln Gln Pro Pro Asn Ser Phe Ser Gln Gln His Ser Glu

50 55 60

Thr Gln Gly Ala Glu Lys Pro Asp Pro Glu Ser Ser His Ser Pro Pro
65 70 75 80

Arg Tyr Thr Asp Gln Gly Gly Glu Glu Glu Glu Asp Tyr Glu Ser Glu
85 90 95

Glu Gln Leu Gln His Arg Ile Leu Thr Ala Ala Leu Glu Phe Val Pro
100 105 110

Ala His Gly Trp Thr Ala Glu Ala Ile Ala Glu Gly Ala Gln Val Cys
115 120 125

Ile Gly Glu Gly Gly Ala Thr
130 135

<210> 141
<211> 2934
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (10)..(804)

<400> 141
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Met Ala Ala Ala Ala Gly Arg Ser Leu Leu Leu Leu Leu Ser
1 5 10

tct cgg ggc ggc ggc ggc ggg ggc gcc ggc ggc tgc ggg gcg ctg act 99

Ser Arg Gly Gly Gly Gly Gly Gly Ala Gly Gly Cys Gly Ala Leu Thr

15 20 25 30

gcc ggc tgc ttc cct ggg ctg ggc gtc agc cgc cac cgg cag cag cag 147

Ala Gly Cys Phe Pro Gly Leu Gly Val Ser Arg His Arg Gln Gln Gln

35 40 45

cac cac cgg acg gta cac cag agg atc gct tcc tgg cag aat ttg gga 195

His His Arg Thr Val His Gln Arg Ile Ala Ser Trp Gln Asn Leu Gly

50 55 60

gct gtt tat tgc agc act gtt gtg ccc tct gat gat gtt aca gtg gtt 243

Ala Val Tyr Cys Ser Thr Val Val Pro Ser Asp Asp Val Thr Val Val

65 70 75

tat caa aat ggg tta cct gtg ata tct gtg agg cta cca tcc cgg cgt 291

Tyr Gln Asn Gly Leu Pro Val Ile Ser Val Arg Leu Pro Ser Arg Arg

80 85 90

gaa cgc tgt cag ttc aca ctc aag cct atc tct gac tct gtt ggt gta 339

Glu Arg Cys Gln Phe Thr Leu Lys Pro Ile Ser Asp Ser Val Gly Val

95 100 105 110

ttt tta cga caa ctg caa gaa gag gat cgg gga att gac aga gtt gct 387

Phe Leu Arg Gln Leu Gln Glu Glu Asp Arg Gly Ile Asp Arg Val Ala

115 120 125

atc tat tca cca gat ggt gtt cgc gtt gct gct tca aca gga ata gac 435
 Ile Tyr Ser Pro Asp Gly Val Arg Val Ala Ala Ser Thr Gly Ile Asp
 130 135 140

ctc ctc ctc ctt gat gac ttt aag ctg gtc att aat gac tta aca tac 483
 Leu Leu Leu Leu Asp Asp Phe Lys Leu Val Ile Asn Asp Leu Thr Tyr
 145 150 155

cac gta cga cca cca aaa aga gac ctc tta agt cat gaa aat gca gca 531
 His Val Arg Pro Pro Lys Arg Asp Leu Leu Ser His Glu Asn Ala Ala
 160 165 170

acg ctg aat gat gta aag aca ttg gtc cag cag cta tac acc aca ctg 579
 Thr Leu Asn Asp Val Lys Thr Leu Val Gln Gln Leu Tyr Thr Thr Leu
 175 180 185 190

tgc att gag cag cac cag tta aac aag gaa agg gag ctt att gaa aga 627
 Cys Ile Glu Gln His Gln Leu Asn Lys Glu Arg Glu Leu Ile Glu Arg
 195 200 205

cta gag gat ctc aaa gag cag ctg gct ccc ctg gaa aag gta cga att 675
 Leu Glu Asp Leu Lys Glu Gln Leu Ala Pro Leu Glu Lys Val Arg Ile
 210 215 220

gag att agc aga aaa gct gag aag agg acc act ttg gtg cta tgg gtg 723
 Glu Ile Ser Arg Lys Ala Glu Lys Arg Thr Thr Leu Val Leu Trp Val
 225 230 235

gcc ttg cct aca tgg cca cac agt ttg gca ttt tgg ccc ggc tta cct 771

Ala Leu Pro Thr Trp Pro His Ser Leu Ala Phe Trp Pro Gly Leu Pro

240

245

250

ggt ggg aat att cct ggg aca tca tgg agc cag taacatactt catcacttat 824

Gly Gly Asn Ile Pro Gly Thr Ser Trp Ser Gln

255

260

265

ggaagtgcc a tggcaatgta tgcataTTTT gtaatgacac gccaggaata tgtttatcca 884

gaagccagag acagacaata ctactatTTT ttccataaag gagccaaaaa gtcacgtttt 944

gacctagaga aatacaatca actcaaggat gcaattgctc aggcagaaat ggaccttaag 1004

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tagaaaagca aattctcatg atatgctaaa atatcattag catttatatt aaattggacc 1544

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ataatcccct ctccctccag aacacaaatc agagggaag ggggtgttca gctgtactac 1904

caaatcagga agatgtaagg ttacaaatt ggctaagaat catggctctg tagccatctc 1964

aaccagaata attttattgc taatctgctt tgtgtgacag cattccaggc cagccagatg 2024

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gagccctccc acctccacaa cttcagttgt aaatcaagtg tgtggatctc aaagggtgca 2144

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atTTTTtctt atcttaaatt gagagaaaga gaattaatct tatactttgt caaaacattt 2264

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ggaggacatg gagaaaagtt cttaaaca atagcaaaact attgaacatg tgtaaaatcc 2864

tgtatcattt atgaaatatg tataaaaagc aatgtacctt ctggaacaat aaatacttat 2924

tcaatttttg 2934

<210> 142

<211> 265

<212> PRT

<213> Homo sapiens

<400> 142

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Gly Gly Gly Gly Gly Gly Ala Gly Gly Cys Gly Ala Leu Thr Ala Gly

20 25 30

Cys Phe Pro Gly Leu Gly Val Ser Arg His Arg Gln Gln Gln His His

35 40 45

Arg Thr Val His Gln Arg Ile Ala Ser Trp Gln Asn Leu Gly Ala Val

50 55 60

Tyr Cys Ser Thr Val Val Pro Ser Asp Asp Val Thr Val Val Tyr Gln

65 70 75 80

Asn Gly Leu Pro Val Ile Ser Val Arg Leu Pro Ser Arg Arg Glu Arg

85 90 95

Cys Gln Phe Thr Leu Lys Pro Ile Ser Asp Ser Val Gly Val Phe Leu

100 105 110

Arg Gln Leu Gln Glu Glu Asp Arg Gly Ile Asp Arg Val Ala Ile Tyr

115 120 125

Ser Pro Asp Gly Val Arg Val Ala Ala Ser Thr Gly Ile Asp Leu Leu

130 135 140

Leu Leu Asp Asp Phe Lys Leu Val Ile Asn Asp Leu Thr Tyr His Val

145 150 155 160

Arg Pro Pro Lys Arg Asp Leu Leu Ser His Glu Asn Ala Ala Thr Leu
165 170 175

Asn Asp Val Lys Thr Leu Val Gln Gln Leu Tyr Thr Thr Leu Cys Ile
180 185 190

Glu Gln His Gln Leu Asn Lys Glu Arg Glu Leu Ile Glu Arg Leu Glu
195 200 205

Asp Leu Lys Glu Gln Leu Ala Pro Leu Glu Lys Val Arg Ile Glu Ile
210 215 220

Ser Arg Lys Ala Glu Lys Arg Thr Thr Leu Val Leu Trp Val Ala Leu
225 230 235 240

Pro Thr Trp Pro His Ser Leu Ala Phe Trp Pro Gly Leu Pro Gly Gly
245 250 255

Asn Ile Pro Gly Thr Ser Trp Ser Gln
260 265

<210> 143

<211> 1658

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (57)..(947)

<400> 143

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Met

1

gag ccg cgg gcg ctc gtc acg gcg ctc agc ctc ggc ctc agc ctg tgc 107

Glu Pro Arg Ala Leu Val Thr Ala Leu Ser Leu Gly Leu Ser Leu Cys

5

10

15

tcc ctg ggg ctg ctc gtc acg gcc atc ttc acc gac cac tgg tac gag 155

Ser Leu Gly Leu Leu Val Thr Ala Ile Phe Thr Asp His Trp Tyr Glu

20

25

30

acc gac ccc cgg cgc cac aag gag agc tgc gag cgc agc cgc gcg ggc 203

Thr Asp Pro Arg Arg His Lys Glu Ser Cys Glu Arg Ser Arg Ala Gly

35

40

45

gcc gac ccc ccg gac cag aag aac cgc ctg atg ccg ctg tcg cac ctg 251

Ala Asp Pro Pro Asp Gln Lys Asn Arg Leu Met Pro Leu Ser His Leu

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ccg ctg cgg gac tcg ccc ccg ctg ggg cgc cgg ctg ctc ccg ggc ggc 299

Pro Leu Arg Asp Ser Pro Pro Leu Gly Arg Arg Leu Leu Pro Gly Gly

70

75

80

ccg ggg cgc gcc gac ccc gag tcc tgg cgc tcg ctc ctg ggg ctc ggc 347

Pro Gly Arg Ala Asp Pro Glu Ser Trp Arg Ser Leu Leu Gly Leu Gly

85

90

95

ggg ctg gac gcc gag tgc ggc cgg ccc ctc ttc gcc acc tac tcg ggc 395

Gly Leu Asp Ala Glu Cys Gly Arg Pro Leu Phe Ala Thr Tyr Ser Gly

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105

110

ctc tgg agg aag tgc tac ttc ctg ggc atc gac cgg gac atc gac acc 443

Leu Trp Arg Lys Cys Tyr Phe Leu Gly Ile Asp Arg Asp Ile Asp Thr

115

120

125

ctc atc ctg aaa ggt att gcg cag cga tgc acg gcc atc aag tac cac 491

Leu Ile Leu Lys Gly Ile Ala Gln Arg Cys Thr Ala Ile Lys Tyr His

130

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ttt tct cag ccc atc cgc ttg cga aac att cct ttt aat tta acc aag 539

Phe Ser Gln Pro Ile Arg Leu Arg Asn Ile Pro Phe Asn Leu Thr Lys

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acc ata cag caa gat gag tgg cac ctg ctt cat tta aga aga atc act 587

Thr Ile Gln Gln Asp Glu Trp His Leu Leu His Leu Arg Arg Ile Thr

165

170

175

gct ggc ttc ctc ggc atg gcc gta gcc gtc ctt ctc tgc ggc tgc att 635

Ala Gly Phe Leu Gly Met Ala Val Ala Val Leu Leu Cys Gly Cys Ile

180

185

190

gtg gcc aca gtc agt ttc ttc tgg gag gag agc ttg acc cag cac gtg 683

Val Ala Thr Val Ser Phe Phe Trp Glu Glu Ser Leu Thr Gln His Val

195

200

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Ala Gly Leu Leu Phe Leu Met Thr Gly Ile Phe Cys Thr Ile Ser Leu

210 215 220 225

tgt act tat gcc gcc agt atc tcg tat gat ttg aac cgg ctc cca aag 779

Cys Thr Tyr Ala Ala Ser Ile Ser Tyr Asp Leu Asn Arg Leu Pro Lys

230 235 240

cta att tat agc ctg cct gct gat gtg gaa cat ggt tac agc tgg tcc 827

Leu Ile Tyr Ser Leu Pro Ala Asp Val Glu His Gly Tyr Ser Trp Ser

245 250 255

atc ttt tgc gcc tgg tgc agt tta ggc ttt att gtg gca gct gga ggt 875

Ile Phe Cys Ala Trp Cys Ser Leu Gly Phe Ile Val Ala Ala Gly Gly

260 265 270

ctc tgc atc gct tat ccg ttt att agc cgg acc aag att gca cag cta 923

Leu Cys Ile Ala Tyr Pro Phe Ile Ser Arg Thr Lys Ile Ala Gln Leu

275 280 285

aag tct ggc aga gac tcc acg gta tgactgtcct cactgggcct gtccacagt 977

Lys Ser Gly Arg Asp Ser Thr Val

290 295

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acattccaac ctgttgctg ccagcccttt ctggattact gatagaaaat catgcaaac 1097

ctcccaacct ttctaaggac aagactactg tggattcaag tgctttaatg actatttatg 1157

cgttgactgt gagaataggg agcagtgcca tgggacattt ctaggtgtag agaaagaaga 1217

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<212> PRT

<213> Homo sapiens

<400> 144

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Cys Ser Leu Gly Leu Leu Val Thr Ala Ile Phe Thr Asp His Trp Tyr

20

25

30

Glu Thr Asp Pro Arg Arg His Lys Glu Ser Cys Glu Arg Ser Arg Ala

35

40

45

Gly Ala Asp Pro Pro Asp Gln Lys Asn Arg Leu Met Pro Leu Ser His

50

55

60

Leu Pro Leu Arg Asp Ser Pro Pro Leu Gly Arg Arg Leu Leu Pro Gly

65

70

75

80

Gly Pro Gly Arg Ala Asp Pro Glu Ser Trp Arg Ser Leu Leu Gly Leu

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95

Gly Gly Leu Asp Ala Glu Cys Gly Arg Pro Leu Phe Ala Thr Tyr Ser

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Gly Leu Trp Arg Lys Cys Tyr Phe Leu Gly Ile Asp Arg Asp Ile Asp

115

120

125

Thr Leu Ile Leu Lys Gly Ile Ala Gln Arg Cys Thr Ala Ile Lys Tyr

130

135

140

His Phe Ser Gln Pro Ile Arg Leu Arg Asn Ile Pro Phe Asn Leu Thr

145

150

155

160

Lys Thr Ile Gln Gln Asp Glu Trp His Leu Leu His Leu Arg Arg Ile

165

170

175

Thr Ala Gly Phe Leu Gly Met Ala Val Ala Val Leu Leu Cys Gly Cys

180

185

190

Ile Val Ala Thr Val Ser Phe Phe Trp Glu Glu Ser Leu Thr Gln His

195

200

205

Val Ala Gly Leu Leu Phe Leu Met Thr Gly Ile Phe Cys Thr Ile Ser

210

215

220

Leu Cys Thr Tyr Ala Ala Ser Ile Ser Tyr Asp Leu Asn Arg Leu Pro

225

230

235

240

Lys Leu Ile Tyr Ser Leu Pro Ala Asp Val Glu His Gly Tyr Ser Trp

245

250

255

Ser Ile Phe Cys Ala Trp Cys Ser Leu Gly Phe Ile Val Ala Ala Gly

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Gly Leu Cys Ile Ala Tyr Pro Phe Ile Ser Arg Thr Lys Ile Ala Gln

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Leu Lys Ser Gly Arg Asp Ser Thr Val

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<222> (71)..(790)

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Met Thr Ala Pro Val Pro Ala Pro Arg Ile Leu Leu Pro

1 5 10

ttg ctg ttg ctg ctg ctg cta acg ccg cct ccg ggt gca cgt ggt gag 157

Leu Leu Leu Leu Leu Leu Leu Thr Pro Pro Pro Gly Ala Arg Gly Glu

15 20 25

gtg tgt atg gct tcc cgt gga ctc agc ctc ttc ccc gag tcc tgt cca 205

Val Cys Met Ala Ser Arg Gly Leu Ser Leu Phe Pro Glu Ser Cys Pro

30 35 40 45

gat ttc tgc tgt ggt acc tgt gat gac caa tac tgc tgc tct gac gtg 253

Asp Phe Cys Cys Gly Thr Cys Asp Asp Gln Tyr Cys Cys Ser Asp Val

50 55 60

ctg aag aaa ttt gtg tgg agc gag gaa agg tgt gct gtg cct gag gcc 301

Leu Lys Lys Phe Val Trp Ser Glu Glu Arg Cys Ala Val Pro Glu Ala

65 70 75

agc gtg cct gcc agt gta gag ccg gtg gag cag ctg ggc tcg gcg ctg 349
Ser Val Pro Ala Ser Val Glu Pro Val Glu Gln Leu Gly Ser Ala Leu

80

85

90

agg ttt cgc cct ggc tac aac gac ccc atg tca ggg ttc gga gcg acc 397

Arg Phe Arg Pro Gly Tyr Asn Asp Pro Met Ser Gly Phe Gly Ala Thr

95

100

105

ttg gcc gtt ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc 445
Leu Ala Val Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile

110

115

120

125

atc tgc ttc acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga 493
Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg

130

135

140

cca cgt ccg gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc 541
Pro Arg Pro Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala

145

150

155

cct tat cct cag cct cca agt gtg ccg ccc agc tac cct gga cca agc 589
Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser

160

165

170

tac cag ggc tac cac acc atg ccg cct cag cca ggg atg cca gca gca 637
Tyr Gln Gly Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala

175

180

185

ccc tac cca atg cag tac cca cca cct tac cca gcc cag ccc atg ggc 685
 Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly
 190 195 200 205

cca ccg gcc tac cac gag acc ctg gct gga gga gca gcc gcg ccc tac 733
 Pro Pro Ala Tyr His Glu Thr Leu Ala Gly Gly Ala Ala Ala Pro Tyr

210

215

220

ccc gcc agc cag cct cct tac aac ccg gcc tac atg gat gcc ccg aag 781
 Pro Ala Ser Gln Pro Pro Tyr Asn Pro Ala Tyr Met Asp Ala Pro Lys
 225 230 235

gcg gcc ctc tgagcattcc ctggcctctc tggctgccac ttggttatgt 830
 Ala Ala Leu
 240

tgtgtgtgtg cgtgagtggg gtgcaggcgc gggttccttac gcccattgtg tgctgtgtgt 890

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ctcgtgttcc tcctccctct attactgttt caccagagct gtcttagctc aaatctgttg 1970

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<212> PRT

<213> Homo sapiens

<400> 146

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Leu Leu Leu Leu Thr Pro Pro Pro Gly Ala Arg Gly Glu Val Cys Met

20 25 30

Ala Ser Arg Gly Leu Ser Leu Phe Pro Glu Ser Cys Pro Asp Phe Cys

35 40 45

Cys Gly Thr Cys Asp Asp Gln Tyr Cys Cys Ser Asp Val Leu Lys Lys

50 55 60

Phe Val Trp Ser Glu Glu Arg Cys Ala Val Pro Glu Ala Ser Val Pro

65 70 75 80

Ala Ser Val Glu Pro Val Glu Gln Leu Gly Ser Ala Leu Arg Phe Arg

85 90 95

Pro Gly Tyr Asn Asp Pro Met Ser Gly Phe Gly Ala Thr Leu Ala Val

100 105 110

Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys Phe

115 120 125

Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg Pro
130 135 140

Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr Pro
145 150 155 160

Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln Gly
165 170 175

Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr Pro
180 185 190

Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro Ala
195 200 205

Tyr His Glu Thr Leu Ala Gly Gly Ala Ala Ala Pro Tyr Pro Ala Ser
210 215 220

Gln Pro Pro Tyr Asn Pro Ala Tyr Met Asp Ala Pro Lys Ala Ala Leu
225 230 235 240

<210> 147

<211> 1898

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (403)..(834)

<400> 147

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caaaaaggga gaaacaaaac agatgagaca agaaaggaaac atccagcatg ctgtgaaccc 180

cctgagactg gccatgatct gaaagagtaa agctctatcc agggaacctt ttctgaatca 240

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gcaatctact gccatggcca catcctgaat gttgacaata ccctaaactg tgccatttat 360

aagatctctg acacaccaac ctctctcctc ttacagctct ca atg atg tat atg 414

Met Met Tyr Met

1

acc tca gct tat tct aat atg ctt aca gat tat aca ccc gtg ata ttg 462

Thr Ser Ala Tyr Ser Asn Met Leu Thr Asp Tyr Thr Pro Val Ile Leu

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15

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atg gca gtg gct gct gct gtc gtg gct gct gct atc acg cct gct gca 510

Met Ala Val Ala Ala Ala Val Val Ala Ala Ala Ile Thr Pro Ala Ala

25

30

35

aca cag agg tgc gac tgg ggc tgc aca ttt cac gga ggt gtt ggg agt 558

Thr Gln Arg Cys Asp Trp Gly Cys Thr Phe His Gly Gly Val Gly Ser

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tcc gcc cct tct gat gtg ggg aaa gag atc ccc agg tgc ccc tgc atc 606

Ser Ala Pro Ser Asp Val Gly Lys Glu Ile Pro Arg Cys Pro Cys Ile

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60

65

tgc cca aac tgt ggc tgt gga tcg gag gct cca ggt tgg cag gtt ggg 654

Cys Pro Asn Cys Gly Cys Gly Ser Glu Ala Pro Gly Trp Gln Val Gly

70

75

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agc ttc cgg gtg cag ctg cga ccg ccc tcc cag gtg cag gac cct ggt 702

Ser Phe Arg Val Gln Leu Arg Pro Pro Ser Gln Val Gln Asp Pro Gly

85

90

95

100

gtt tct gca gcc tgc acc ctt ggg ggc ccc agg aaa gac cca tat cct 750

Val Ser Ala Ala Cys Thr Leu Gly Gly Pro Arg Lys Asp Pro Tyr Pro

105

110

115

tgc agg ctt gga ggt gtt tgc ttc ttc tgc ctg gcc tct ctc ggc tcc 798

Cys Arg Leu Gly Gly Val Cys Phe Phe Cys Leu Ala Ser Leu Gly Ser

120

125

130

cgg tgc atg ctc tca tat ctg agt ggg ggt tgg tgc tgagccccgg 844

Arg Cys Met Leu Ser Tyr Leu Ser Gly Gly Trp Cys

135

140

ggccgtgaat tgcagcagga ggcagattta ttcctgggca gaagggtggca gatcccaagt 904

aaggggacct tcaagccagg gagggcctga aggctggtgg ctgggctacc agtcccaccg 964

accagagtgg ggattcgtgg gcctcttctg ggccacccat agccacccat ggaccaatca 1024

gcaagcacat cctccccctct gaggtccgta aaagccctgg gcgcagcctg agcagggcag 1084

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actgactcct tatctcagtt atgttatgtg ttaaattgtt acagtgttat tttgtatctc 1804

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tggtataagt aaataaaaaat aagtctgaat ggcc 1898

<210> 148

<211> 144

<212> PRT

<213> Homo sapiens

<400> 148

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1 5 10 15

Pro Val Ile Leu Met Ala Val Ala Ala Val Val Ala Ala Ala Ile

20 25 30

Thr Pro Ala Ala Thr Gln Arg Cys Asp Trp Gly Cys Thr Phe His Gly

35 40 45

Gly Val Gly Ser Ser Ala Pro Ser Asp Val Gly Lys Glu Ile Pro Arg

50 55 60

Cys Pro Cys Ile Cys Pro Asn Cys Gly Cys Gly Ser Glu Ala Pro Gly

65 70 75 80

Trp Gln Val Gly Ser Phe Arg Val Gln Leu Arg Pro Pro Ser Gln Val

85 90 95

Gln Asp Pro Gly Val Ser Ala Ala Cys Thr Leu Gly Gly Pro Arg Lys

100

105

110

Asp Pro Tyr Pro Cys Arg Leu Gly Gly Val Cys Phe Phe Cys Leu Ala

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120

125

Ser Leu Gly Ser Arg Cys Met Leu Ser Tyr Leu Ser Gly Gly Trp Cys

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135

140

<210> 149

<211> 1755

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (201)..(1166)

<400> 149

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ggactagtta ttgagcatct gcctctcata tcaccagtgg ccatctgagg tgtttccctg 180

gctctgaagg ggtaggcacg atg gcc agg tgc ttc agc ctg gtg ttg ctt ctc 233

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu

1

5

10

act tcc atc tgg acc acg agg ctc ctg gtc caa ggc tct ttg cgt gca 281

Thr Ser Ile Trp Thr Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala

15

20

25

gaa gag ctt tcc atc cag gtg tca tgc aga att atg ggg atc acc ctt 329

Glu Glu Leu Ser Ile Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu

30

35

40

gtg agc aaa aag gcg aac cag cag ctg aat ttc aca gaa gct aag gag 377

Val Ser Lys Lys Ala Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu

45

50

55

gcc tgt agg ctg ctg gga cta agt ttg gcc ggc aag gac caa gtt gaa 425

Ala Cys Arg Leu Leu Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu

60

65

70

75

aca gcc ttg aaa gct agc ttt gaa act tgc agc tat ggc tgg gtt gga 473

Thr Ala Leu Lys Ala Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly

80

85

90

gat gga ttc gtg gtc atc tct agg att agc cca aac ccc aag tgt ggg 521

Asp Gly Phe Val Val Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly

95

100

105

aaa aat ggg gtg ggt gtc ctg att tgg aag gtt cca gtg agc cga cag 569

Lys Asn Gly Val Gly Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln

110

115

120

ttt gca gcc tat tgt tac aac tca tct gat act tgg act aac tcg tgc 617
Phe Ala Ala Tyr Cys Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys
125 130 135

att cca gaa att atc acc acc aaa gat ccc ata ttc aac act caa act 665
Ile Pro Glu Ile Ile Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr

140 145 150 155

gca aca caa aca aca gaa ttt att gtc agt gac agt acc tac tcg gtg 713
Ala Thr Gln Thr Thr Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val
160 165 170

gca tcc cct tac tct aca ata cct gcc cct act act act cct cct gct 761
Ala Ser Pro Tyr Ser Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala
175 180 185

cca gct tcc act tct att cca cgg aga aaa aaa ttg att tgt gtc aca 809
Pro Ala Ser Thr Ser Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr
190 195 200

gaa gtt ttt atg gaa act agc acc atg tct aca gaa act gaa cca ttt 857
Glu Val Phe Met Glu Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe
205 210 215

gtt gaa aat aaa gca gca ttc aag aat gaa gct gct ggg ttt gga ggt 905
Val Glu Asn Lys Ala Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly
220 225 230 235

gtc ccc acg gct ctg cta gtg ctt gct ctc ctc ttc ttt ggt gct gca 953

Val Pro Thr Ala Leu Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala
240 245 250

gct ggt ctt gga ttt tgc tat gtc aaa agg tat gtg aag gcc ttc cct 1001
Ala Gly Leu Gly Phe Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro
255 260 265

ttt aca aac aag aat cag cag aag gaa atg atc gaa acc aaa gta gta 1049
Phe Thr Asn Lys Asn Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val
270 275 280

aag gag gag aag gcc aat gat agc aac cct aat gag gaa tca aag aaa 1097
Lys Glu Glu Lys Ala Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys
285 290 295

act gat aaa aac cca gaa gag tcc aag agt cca agc aaa act acc gtg 1145
Thr Asp Lys Asn Pro Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val
300 305 310 315

cga tgc ctg gaa gct gaa gtt tagatgagac agaaatgagg agacacacct 1196
Arg Cys Leu Glu Ala Glu Val
320

gaggctggtt tctttcatgc tccttaccct gccccagctg gggaaatcaa aagggccaaa 1256

gaaccaaaga agaaagtcca cccttggttc ctaactggaa tcagctcagg actgccattg 1316

gactatggag tgcaccaaag agaatgccct tctccttatt gtaaccctgt ctggatccta 1376

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aataaagaaa tagaacaag 1755

<210> 150

<211> 322

<212> PRT

<213> Homo sapiens

<400> 150

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Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala

35 40 45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu

50

55

60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala

65

70

75

80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val

85

90

95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly

100

105

110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys

115

120

125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile

130

135

140

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr

145

150

155

160

Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser

165

170

175

Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser

180

185

190

Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu

195

200

205

Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala

210

215

220

Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu

225

230

235

240

Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe

245

250

255

Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn

260

265

270

Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala

275

280

285

Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro

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Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala

305

310

315

320

Glu Val

<210> 151

<211> 1907

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (21)..(1196)

<400> 151

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Met Glu Trp Trp Ala Ser Ser Pro Leu Arg Leu

1 5 10

tgg ctg ctg ttg ttc ctc ctg ccc tca gcg cag ggc cgc cag aag gag 101

Trp Leu Leu Leu Phe Leu Leu Pro Ser Ala Gln Gly Arg Gln Lys Glu

15 20 25

tca ggt tca aaa tgg aaa gta ttt att gac caa att aac agg tct ttg 149

Ser Gly Ser Lys Trp Lys Val Phe Ile Asp Gln Ile Asn Arg Ser Leu

30 35 40

gag aat tac gaa cca tgt tca agt caa aac tgc agc tgc tac cat ggt 197

Glu Asn Tyr Glu Pro Cys Ser Ser Gln Asn Cys Ser Cys Tyr His Gly

45 50 55

gtc ata gaa gag gat cta act cct ttc cga gga ggc atc tcc agg aag 245

Val Ile Glu Glu Asp Leu Thr Pro Phe Arg Gly Gly Ile Ser Arg Lys

60 65 70 75

atg atg gca gag gta gtc aga cgg aag cta ggg acc cac tat cag atc 293

Met Met Ala Glu Val Val Arg Arg Lys Leu Gly Thr His Tyr Gln Ile

80

85

90

act aag aac aga ctg tac cgg gaa aat gac tgc atg ttc ccc tca agg 341

Thr Lys Asn Arg Leu Tyr Arg Glu Asn Asp Cys Met Phe Pro Ser Arg

95

100

105

tgt agt ggt gtt gag cac ttt att ttg gaa gtg atc ggg cgt ctc cct 389

Cys Ser Gly Val Glu His Phe Ile Leu Glu Val Ile Gly Arg Leu Pro

110

115

120

gac atg gag atg gtg atc aat gta cga gat tat cct cag gtt cct aaa 437

Asp Met Glu Met Val Ile Asn Val Arg Asp Tyr Pro Gln Val Pro Lys

125

130

135

tgg atg gag cct gcc atc cca gtc ttc tcc ttc agt aag aca tca gag 485

Trp Met Glu Pro Ala Ile Pro Val Phe Ser Phe Ser Lys Thr Ser Glu

140

145

150

155

tac cat gat atc atg tat cct gct tgg aca ttt tgg gaa ggg gga cct 533

Tyr His Asp Ile Met Tyr Pro Ala Trp Thr Phe Trp Glu Gly Gly Pro

160

165

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gct gtt tgg cca att tat cct aca ggt ctt gga cgg tgg gac ctc ttc 581

Ala Val Trp Pro Ile Tyr Pro Thr Gly Leu Gly Arg Trp Asp Leu Phe

175

180

185

aga gaa gat ctg gta agg tca gca gca cag tgg cca tgg aaa aag aaa 629

Arg Glu Asp Leu Val Arg Ser Ala Ala Gln Trp Pro Trp Lys Lys Lys

190

195

200

aac tct aca gca tat ttc cga gga tca agg aca agt cca gaa cga gat 677

Asn Ser Thr Ala Tyr Phe Arg Gly Ser Arg Thr Ser Pro Glu Arg Asp

205

210

215

cct ctc att ctt ctg tct cgg aaa aac cca aaa ctt gtt gat gca gaa 725

Pro Leu Ile Leu Leu Ser Arg Lys Asn Pro Lys Leu Val Asp Ala Glu

220

225

230

235

tac acc aaa aac cag gcc tgg aaa tct atg aaa gat acc tta gga aag 773

Tyr Thr Lys Asn Gln Ala Trp Lys Ser Met Lys Asp Thr Leu Gly Lys

240

245

250

cca gct gct aag gat gtc cat ctt gtg gat cac tgc aaa tac aag tac 821

Pro Ala Ala Lys Asp Val His Leu Val Asp His Cys Lys Tyr Lys Tyr

255

260

265

ctg ttt aat ttt cga ggc gta gct gca agt ttc cgg ttt aaa cac ctc 869

Leu Phe Asn Phe Arg Gly Val Ala Ala Ser Phe Arg Phe Lys His Leu

270

275

280

ttc ctg tgt ggc tca ctt gtt ttc cat gtt ggt gat gag tgg cta gaa 917

Phe Leu Cys Gly Ser Leu Val Phe His Val Gly Asp Glu Trp Leu Glu

285

290

295

ttc ttc tat cca cag ctg aag cca tgg gtt cac tat atc cca gtc aaa 965

Phe Phe Tyr Pro Gln Leu Lys Pro Trp Val His Tyr Ile Pro Val Lys

300

305

310

315

aca gat ctc tcc aat gtc caa gag ctg tta caa ttt gta aaa gca aat 1013

Thr Asp Leu Ser Asn Val Gln Glu Leu Leu Gln Phe Val Lys Ala Asn

320

325

330

gat gat gta gct caa gag att gct gaa agg gga agc cag ttt att agg 1061

Asp Asp Val Ala Gln Glu Ile Ala Glu Arg Gly Ser Gln Phe Ile Arg

335

340

345

aac cat ttg cag atg gat gac atc acc tgt tac tgg gag aac ctc ttg 1109

Asn His Leu Gln Met Asp Asp Ile Thr Cys Tyr Trp Glu Asn Leu Leu

350

355

360

agt gaa tac tct aaa ttc ctg tct tat aat gta acg aga agg aaa ggt 1157

Ser Glu Tyr Ser Lys Phe Leu Ser Tyr Asn Val Thr Arg Arg Lys Gly

365

370

375

tat gat caa att att ccc aaa atg ttg aaa act gaa cta tagtagtcat 1206

Tyr Asp Gln Ile Ile Pro Lys Met Leu Lys Thr Glu Leu

380

385

390

cataggacca tagtcctctt tgtggcaaca gatctcagat atcctacggt gagaagctta 1266

ccataagctt ggcacctata ccttgaatat ctgctatcaa gccaaatacc tggttttcct 1326

tatcatgctg caccagagc aactcttgag aaagatttaa aatgtgtcta atacactgat 1386

atgaagcagt tcaacttttt ggatgaataa ggaccagaaa tcgtgagatg tggattttga 1446

acccaactct acctttcatt ttcttaagac caatcacagc ttgtgcctca gatcatccac 1506

ctgtgtgagt ccatcactgt gaaattgact gtgtccatgt gatgatgcc tttgtcccat 1566

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ttattcaagg cgtgatctct gtcactttat tttaatgtag gaaaccctat ggggtttatg 1686

aaaaatactt ggggatcatt ctctgaatgg tctaaggaag cggtagccat gccatgcaat 1746

gatgtaggag ttctcttttg taaaaccata aactgtgta ctcaggaggt ttctataatg 1806

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ttgtgccttc atgccctact tcttaatgcc tctctaaagc c 1907

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<211> 392

<212> PRT

<213> Homo sapiens

<400> 152

Met Glu Trp Trp Ala Ser Ser Pro Leu Arg Leu Trp Leu Leu Leu Phe

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Leu Leu Pro Ser Ala Gln Gly Arg Gln Lys Glu Ser Gly Ser Lys Trp

20

25

30

Lys Val Phe Ile Asp Gln Ile Asn Arg Ser Leu Glu Asn Tyr Glu Pro
35 40 45

Cys Ser Ser Gln Asn Cys Ser Cys Tyr His Gly Val Ile Glu Glu Asp
50 55 60

Leu Thr Pro Phe Arg Gly Gly Ile Ser Arg Lys Met Met Ala Glu Val
65 70 75 80

Val Arg Arg Lys Leu Gly Thr His Tyr Gln Ile Thr Lys Asn Arg Leu
85 90 95

Tyr Arg Glu Asn Asp Cys Met Phe Pro Ser Arg Cys Ser Gly Val Glu
100 105 110

His Phe Ile Leu Glu Val Ile Gly Arg Leu Pro Asp Met Glu Met Val
115 120 125

Ile Asn Val Arg Asp Tyr Pro Gln Val Pro Lys Trp Met Glu Pro Ala
130 135 140

Ile Pro Val Phe Ser Phe Ser Lys Thr Ser Glu Tyr His Asp Ile Met
145 150 155 160

Tyr Pro Ala Trp Thr Phe Trp Glu Gly Gly Pro Ala Val Trp Pro Ile
165 170 175

Tyr Pro Thr Gly Leu Gly Arg Trp Asp Leu Phe Arg Glu Asp Leu Val
180 185 190

Arg Ser Ala Ala Gln Trp Pro Trp Lys Lys Lys Asn Ser Thr Ala Tyr

195

200

205

Phe Arg Gly Ser Arg Thr Ser Pro Glu Arg Asp Pro Leu Ile Leu Leu

210

215

220

Ser Arg Lys Asn Pro Lys Leu Val Asp Ala Glu Tyr Thr Lys Asn Gln

225

230

235

240

Ala Trp Lys Ser Met Lys Asp Thr Leu Gly Lys Pro Ala Ala Lys Asp

245

250

255

Val His Leu Val Asp His Cys Lys Tyr Lys Tyr Leu Phe Asn Phe Arg

260

265

270

Gly Val Ala Ala Ser Phe Arg Phe Lys His Leu Phe Leu Cys Gly Ser

275

280

285

Leu Val Phe His Val Gly Asp Glu Trp Leu Glu Phe Phe Tyr Pro Gln

290

295

300

Leu Lys Pro Trp Val His Tyr Ile Pro Val Lys Thr Asp Leu Ser Asn

305

310

315

320

Val Gln Glu Leu Leu Gln Phe Val Lys Ala Asn Asp Asp Val Ala Gln

325

330

335

Glu Ile Ala Glu Arg Gly Ser Gln Phe Ile Arg Asn His Leu Gln Met

340

345

350

Asp Asp Ile Thr Cys Tyr Trp Glu Asn Leu Leu Ser Glu Tyr Ser Lys

355

360

365

Phe Leu Ser Tyr Asn Val Thr Arg Arg Lys Gly Tyr Asp Gln Ile Ile

370

375

380

Pro Lys Met Leu Lys Thr Glu Leu

385

390

<210> 153

<211> 2981

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (58)..(1770)

<400> 153

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Met Arg Ala Leu Arg Asp Arg Ala Gly Leu Leu Leu Cys Val Leu Leu

1

5

10

15

ctg gcg gcg ctg ctg gag gcg gcg cta ggg ctc ccc gtg aag aag ccg 153

Leu Ala Ala Leu Leu Glu Ala Ala Leu Gly Leu Pro Val Lys Lys Pro

20

25

30

cgg ctc cgc gga cca cgg cct ggg agc ctc acg agg ctc gca gag gtc 201

Arg Leu Arg Gly Pro Arg Pro Gly Ser Leu Thr Arg Leu Ala Glu Val

35

40

45

tca gcc tcc cca gat cct agg cct ctg aag gaa gag gag gag gca cca 249

Ser Ala Ser Pro Asp Pro Arg Pro Leu Lys Glu Glu Glu Glu Ala Pro

50

55

60

ctg ctc ccc aga acc cac ctg cag gca gag cca cac caa cat gga tgc 297

Leu Leu Pro Arg Thr His Leu Gln Ala Glu Pro His Gln His Gly Cys

65

70

75

80

tgg act gtc act gag cca gca gcc atg acc cca ggc aac acc acc cct 345

Trp Thr Val Thr Glu Pro Ala Ala Met Thr Pro Gly Asn Thr Thr Pro

85

90

95

ccc agg acc cca gag gtt act ccg ttg cgg ctg gag ctg cag aag ctg 393

Pro Arg Thr Pro Glu Val Thr Pro Leu Arg Leu Glu Leu Gln Lys Leu

100

105

110

ccg gga ttg gcc agc aca acc ttg agt acc cct aac cct gat acc cag 441

Pro Gly Leu Ala Ser Thr Thr Leu Ser Thr Pro Asn Pro Asp Thr Gln

115

120

125

gct tca gcc tcc cca gat cct agg cct ctg agg gaa gag gag gag gca 489

Ala Ser Ala Ser Pro Asp Pro Arg Pro Leu Arg Glu Glu Glu Glu Ala

130	135	140	
cga ctg ctc ccc aga acc cac ctg cag gca gag cta cac caa cat gga	537		
Arg Leu Leu Pro Arg Thr His Leu Gln Ala Glu Leu His Gln His Gly			
145	150	155	160

tgt tgg act gtc act gag cca gca gcc ctg acc cca ggg aat gcc acg	585		
Cys Trp Thr Val Thr Glu Pro Ala Ala Leu Thr Pro Gly Asn Ala Thr			
165	170	175	

cct ccc agg acc cag gag gtt act ccc ttg ctg ctg gag ctg cag aag	633		
Pro Pro Arg Thr Gln Glu Val Thr Pro Leu Leu Leu Glu Leu Gln Lys			
180	185	190	

ctg cca gaa ttg gtc cac gca acc ttg agt acc cct aac cct gat aac	681		
Leu Pro Glu Leu Val His Ala Thr Leu Ser Thr Pro Asn Pro Asp Asn			
195	200	205	

cag gtg acc atc aag gtg gtg gag gac ccc cag gcc gag gtg tcg ata	729		
Gln Val Thr Ile Lys Val Val Glu Asp Pro Gln Ala Glu Val Ser Ile			
210	215	220	

gac ctg ttg gct gag ccc agc aat ccc ccg ccc cag gat acc ctt agc	777		
Asp Leu Leu Ala Glu Pro Ser Asn Pro Pro Pro Gln Asp Thr Leu Ser			
225	230	235	240

tgg ctg ccc gcc ctc tgg ccc ttc ctc tgg gga gac tac aaa gga gag	825		
Trp Leu Pro Ala Leu Trp Pro Phe Leu Trp Gly Asp Tyr Lys Gly Glu			
245	250	255	

gaa aaa gac agg gcc cca ggg gag aag ggg gag gaa aag gag gaa gac 873

Glu Lys Asp Arg Ala Pro Gly Glu Lys Gly Glu Glu Lys Glu Glu Asp

260

265

270

gag gac tat cct tca gag gat atc gag ggt gag gat caa gag gac aaa 921

Glu Asp Tyr Pro Ser Glu Asp Ile Glu Gly Glu Asp Gln Glu Asp Lys

275

280

285

gag gaa gat gag gaa gag cag gcg ctc tgg ttc aat gga act aca gac 969

Glu Glu Asp Glu Glu Glu Gln Ala Leu Trp Phe Asn Gly Thr Thr Asp

290

295

300

aac tgg gac cag ggc tgg ctg gcc ccc ggg gat tgg gtc ttc aag gat 1017

Asn Trp Asp Gln Gly Trp Leu Ala Pro Gly Asp Trp Val Phe Lys Asp

305

310

315

320

tct gtc agc tac gac tat gag cct cag aag gag tgg agt ccc tgg tct 1065

Ser Val Ser Tyr Asp Tyr Glu Pro Gln Lys Glu Trp Ser Pro Trp Ser

325

330

335

ccc tgc agt ggg aac tgc agc act ggc aag cag cag agg act cgg ccc 1113

Pro Cys Ser Gly Asn Cys Ser Thr Gly Lys Gln Gln Arg Thr Arg Pro

340

345

350

tgt ggc tat ggc tgc act gcc acc gag acc cgt acc tgt gac ctg ccc 1161

Cys Gly Tyr Gly Cys Thr Ala Thr Glu Thr Arg Thr Cys Asp Leu Pro

355

360

365

tcc tgt cct ggc act gag gac aag gac acc ttg ggc ctc ccc agt gag 1209

Ser Cys Pro Gly Thr Glu Asp Lys Asp Thr Leu Gly Leu Pro Ser Glu

370

375

380

gag tgg aag ctc ctg gcc cgc aat gct acg gac atg cat gat caa gat 1257

Glu Trp Lys Leu Leu Ala Arg Asn Ala Thr Asp Met His Asp Gln Asp

385

390

395

400

gtg gac agc tgt gag aag tgg ctg aac tgc aag agc gac ttc cta atc 1305

Val Asp Ser Cys Glu Lys Trp Leu Asn Cys Lys Ser Asp Phe Leu Ile

405

410

415

aag tat ctg agc cag atg ctg cgg gac ctg ccc agc tgc ccg tgt gcc 1353

Lys Tyr Leu Ser Gln Met Leu Arg Asp Leu Pro Ser Cys Pro Cys Ala

420

425

430

tac cca ctg gag gcc atg gac agc cct gtg agc cta cag gac gag cac 1401

Tyr Pro Leu Glu Ala Met Asp Ser Pro Val Ser Leu Gln Asp Glu His

435

440

445

cag ggc cgc agc ttc cgg tgg agg gat gcc agt ggc cct cgc gag cgc 1449

Gln Gly Arg Ser Phe Arg Trp Arg Asp Ala Ser Gly Pro Arg Glu Arg

450

455

460

ctg gac atc tac cag ccc acg gcg cgc ttc tgc ctg cgt tcc atg ctg 1497

Leu Asp Ile Tyr Gln Pro Thr Ala Arg Phe Cys Leu Arg Ser Met Leu

465

470

475

480

tct ggg gag agc agc aca ctg gcc gcc cag cac tgc tgc tat gac gag 1545

Ser Gly Glu Ser Ser Thr Leu Ala Ala Gln His Cys Cys Tyr Asp Glu

485

490

495

gac agc cgg ctg ctg acc cgt ggc aag ggc gcc ggc atg ccc aac ctc 1593

Asp Ser Arg Leu Leu Thr Arg Gly Lys Gly Ala Gly Met Pro Asn Leu

500

505

510

atc agc acc gac ttc tca cct aag ctg cac ttc aag ttc gac acg acg 1641

Ile Ser Thr Asp Phe Ser Pro Lys Leu His Phe Lys Phe Asp Thr Thr

515

520

525

ccc tgg atc ctg tgc aag ggg gac tgg agc cgc ctc cac gct gtg ctc 1689

Pro Trp Ile Leu Cys Lys Gly Asp Trp Ser Arg Leu His Ala Val Leu

530

535

540

cct ccc aac aac ggc cga gcc tgc acc gac aac ccc ctg gag gag gag 1737

Pro Pro Asn Asn Gly Arg Ala Cys Thr Asp Asn Pro Leu Glu Glu Glu

545

550

555

560

tac cta gca cag ttg cag gag gcc aag gag tac tagtgacggg gttgctgaac 1790

Tyr Leu Ala Gln Leu Gln Glu Ala Lys Glu Tyr

565

570

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ggccctcacc cgccctgcc cagacagggt gaggaagggt ctccccagt gaggttggtc 1910

cgaggctgtg tgccctctgc cagcgacccc gaagcagata tctcagtggg gttagtgaga 1970

aggttgaagg gtatgtaggg cccaggggtg gtgtccctgg gagccctgga aatgtgcata 2030

tgtgcatgtg tctgccgggg cctccctctg ctgcctgctg ggaccctggc cactcatttt 2090

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gaatgggttg cccaattctg gtccctttcc tttgctcagc cccctctgtt ctgctgattg 2510

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gcctcccat tcccctggct gcacttcctt gccttctatg gggttgaaat gttgaagtct 2870

caactgtctc tgttcacaag agccaccaaa agttagggga cttcagtect agccccaga 2930

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<210> 154

<211> 571

<212> PRT

<213> Homo sapiens

<400> 154

Met Arg Ala Leu Arg Asp Arg Ala Gly Leu Leu Leu Cys Val Leu Leu

1 5 10 15

Leu Ala Ala Leu Leu Glu Ala Ala Leu Gly Leu Pro Val Lys Lys Pro

20 25 30

Arg Leu Arg Gly Pro Arg Pro Gly Ser Leu Thr Arg Leu Ala Glu Val

35 40 45

Ser Ala Ser Pro Asp Pro Arg Pro Leu Lys Glu Glu Glu Glu Ala Pro

50 55 60

Leu Leu Pro Arg Thr His Leu Gln Ala Glu Pro His Gln His Gly Cys

65 70 75 80

Trp Thr Val Thr Glu Pro Ala Ala Met Thr Pro Gly Asn Thr Thr Pro

85 90 95

Pro Arg Thr Pro Glu Val Thr Pro Leu Arg Leu Glu Leu Gln Lys Leu

100

105

110

Pro Gly Leu Ala Ser Thr Thr Leu Ser Thr Pro Asn Pro Asp Thr Gln

115

120

125

Ala Ser Ala Ser Pro Asp Pro Arg Pro Leu Arg Glu Glu Glu Glu Ala

130

135

140

Arg Leu Leu Pro Arg Thr His Leu Gln Ala Glu Leu His Gln His Gly

145

150

155

160

Cys Trp Thr Val Thr Glu Pro Ala Ala Leu Thr Pro Gly Asn Ala Thr

165

170

175

Pro Pro Arg Thr Gln Glu Val Thr Pro Leu Leu Leu Glu Leu Gln Lys

180

185

190

Leu Pro Glu Leu Val His Ala Thr Leu Ser Thr Pro Asn Pro Asp Asn

195

200

205

Gln Val Thr Ile Lys Val Val Glu Asp Pro Gln Ala Glu Val Ser Ile

210

215

220

Asp Leu Leu Ala Glu Pro Ser Asn Pro Pro Pro Gln Asp Thr Leu Ser

225

230

235

240

Trp Leu Pro Ala Leu Trp Pro Phe Leu Trp Gly Asp Tyr Lys Gly Glu

245

250

255

Glu Lys Asp Arg Ala Pro Gly Glu Lys Gly Glu Glu Lys Glu Glu Asp

260

265

270

Glu Asp Tyr Pro Ser Glu Asp Ile Glu Gly Glu Asp Gln Glu Asp Lys

275

280

285

Glu Glu Asp Glu Glu Glu Gln Ala Leu Trp Phe Asn Gly Thr Thr Asp

290

295

300

Asn Trp Asp Gln Gly Trp Leu Ala Pro Gly Asp Trp Val Phe Lys Asp

305

310

315

320

Ser Val Ser Tyr Asp Tyr Glu Pro Gln Lys Glu Trp Ser Pro Trp Ser

325

330

335

Pro Cys Ser Gly Asn Cys Ser Thr Gly Lys Gln Gln Arg Thr Arg Pro

340

345

350

Cys Gly Tyr Gly Cys Thr Ala Thr Glu Thr Arg Thr Cys Asp Leu Pro

355

360

365

Ser Cys Pro Gly Thr Glu Asp Lys Asp Thr Leu Gly Leu Pro Ser Glu

370

375

380

Glu Trp Lys Leu Leu Ala Arg Asn Ala Thr Asp Met His Asp Gln Asp

385

390

395

400

Val Asp Ser Cys Glu Lys Trp Leu Asn Cys Lys Ser Asp Phe Leu Ile
405 410 415

Lys Tyr Leu Ser Gln Met Leu Arg Asp Leu Pro Ser Cys Pro Cys Ala
420 425 430

Tyr Pro Leu Glu Ala Met Asp Ser Pro Val Ser Leu Gln Asp Glu His
435 440 445

Gln Gly Arg Ser Phe Arg Trp Arg Asp Ala Ser Gly Pro Arg Glu Arg
450 455 460

Leu Asp Ile Tyr Gln Pro Thr Ala Arg Phe Cys Leu Arg Ser Met Leu
465 470 475 480

Ser Gly Glu Ser Ser Thr Leu Ala Ala Gln His Cys Cys Tyr Asp Glu
485 490 495

Asp Ser Arg Leu Leu Thr Arg Gly Lys Gly Ala Gly Met Pro Asn Leu
500 505 510

Ile Ser Thr Asp Phe Ser Pro Lys Leu His Phe Lys Phe Asp Thr Thr
515 520 525

Pro Trp Ile Leu Cys Lys Gly Asp Trp Ser Arg Leu His Ala Val Leu
530 535 540

Pro Pro Asn Asn Gly Arg Ala Cys Thr Asp Asn Pro Leu Glu Glu Glu
545 550 555 560

Tyr Leu Ala Gln Leu Gln Glu Ala Lys Glu Tyr

565

570

<210> 155

<211> 1361

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (169)..(822)

<400> 155

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cgcccctggg accctccggg ccgggcgggtt tggcccctta gcgcccgggc gtcggggcgg 120

taaaaggccg gcagaaggga ggcacttgag gacccaagtt tcttcacc atg ggg atg 177

Met Gly Met

1

tgg tcc att ggt gca gga gcc ctg ggg gct gct gcc ttg gca ttg ctg 225

Trp Ser Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu

5

10

15

ctt gcc aac aca gac gtg ttt ctg tcc aag ccc cag aaa gcg gcc ctg 273

Leu Ala Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu

20	25	30	35
gag tac ctg gag gat ata gac ctg aaa aca ctg gag aag gaa cca agg 321			
Glu Tyr Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg			
40	45	50	
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act ttc aaa gca aag gag cta tgg gaa aaa aat gga gct gtg att atg 369			
Thr Phe Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met			
55	60	65	
gcc gtg cgg agg cca ggc tgt ttc ctc tgt cga gag gaa gct gcg gat 417			
Ala Val Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp			
70	75	80	
ctg tcc tcc ctg aaa agc atg ttg gac cag ctg ggc gtc ccc ctc tat 465			
Leu Ser Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr			
85	90	95	
gca gtg gta aag gag cac atc agg act gaa gtg aag gat ttc cag cct 513			
Ala Val Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro			
100	105	110	115
tat ttc aaa gga gaa atc ttc ctg gat gaa aag aaa aag ttc tat ggt 561			
Tyr Phe Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly			
120	125	130	
cca caa agg cgg aag atg atg ttt atg gga ttt atc cgt ctg gga gtg 609			
Pro Gln Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val			
135	140	145	

tgg tac aac ttc ttc cga gcc tgg aac gga ggc ttc tct gga aac ctg 657

Trp Tyr Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu

150

155

160

gaa gga gaa ggc ttc atc ctt ggg gga gtt ttc gtg gtg gga tca gga 705

Glu Gly Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly

165

170

175

aag cag ggc att ctt ctt gag cac cga gaa aaa gaa ttt gga gac aga 753

Lys Gln Gly Ile Leu Leu Glu His Arg Glu Lys Glu Phe Gly Asp Arg

180

185

190

195

gta aac cta ctt tct gtt ctg gaa gct gct aag atg atc aaa cca cag 801

Val Asn Leu Leu Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro Gln

200

205

210

act ttg gcc tca gag aaa aaa tgattgtgtg aaactgccca gctcaggat 852

Thr Leu Ala Ser Glu Lys Lys

215

aaccaggac attcacctgt gttcatggga tgtattgttt ccactcgtgt ccctaaggag 912

tgagaaacc atttatactc tactctcagt atggattatt aatgtatttt aatattctgt 972

ttaggccac taaggcaaaa tagcccaaaa acaagactga caaaaatctg aaaaactaat 1032

gaggattatt aagctaaaac ctgggaaata ggaggcttaa aattgactgc caggctgggt 1092

gcagtggctc acacctgtaa tcccagcact ttgggaggcc aaggtgagca agtcacttga 1152

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aaaaatcacc cgggtgtggt ggcaggcacc ttagtccca gctacccggg aggctgaggc 1272

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<210> 156

<211> 218

<212> PRT

<213> Homo sapiens

<400> 156

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Ala Leu Leu Leu Ala Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys

20 25 30

Ala Ala Leu Glu Tyr Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys

35 40 45

Glu Pro Arg Thr Phe Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala

50 55 60

Val Ile Met Ala Val Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu
65 70 75 80

Ala Ala Asp Leu Ser Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val
85 90 95

Pro Leu Tyr Ala Val Val Lys Glu His Ile Arg Thr Glu Val Lys Asp
100 105 110

Phe Gln Pro Tyr Phe Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys
115 120 125

Phe Tyr Gly Pro Gln Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg
130 135 140

Leu Gly Val Trp Tyr Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser
145 150 155 160

Gly Asn Leu Glu Gly Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val
165 170 175

Gly Ser Gly Lys Gln Gly Ile Leu Leu Glu His Arg Glu Lys Glu Phe
180 185 190

Gly Asp Arg Val Asn Leu Leu Ser Val Leu Glu Ala Ala Lys Met Ile
195 200 205

Lys Pro Gln Thr Leu Ala Ser Glu Lys Lys
210 215

<210> 157

<211> 1976

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (13)..(387)

<400> 157

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Met Tyr Phe Ile Phe Thr Ser Phe Trp Ala Tyr Lys Ile

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10

tat tat gtc tat ggc ttc atg atg ctg gtg ctg gtt atc ctg tgc att 99

Tyr Tyr Val Tyr Gly Phe Met Met Leu Val Leu Val Ile Leu Cys Ile

15

20

25

gtg act gtc tgt gtg act att gtg tgc aca tat ttt cta cta aat gca 147

Val Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala

30

35

40

45

gaa gat tac agg tgg caa tgg aca agt ttt ctc tct gct gca tca act 195

Glu Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr

50

55

60

gca atc tat gtt tac atg tat tcc ttt tac tac tat ttt ttc aaa aca 243

Ala Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr

65

70

75

aag atg tat ggc tta ttt caa aca tca ttt tac ttt gga tat atg gcg 291

Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala

80

85

90

gta ttt agc aca gcc ttg ggg ata atg tgt gga gcg att ggt tac atg 339

Val Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile Gly Tyr Met

95

100

105

gga aca agt gcc ttt gtc cga aaa atc tat act aat gtg aaa att gac 387

Gly Thr Ser Ala Phe Val Arg Lys Ile Tyr Thr Asn Val Lys Ile Asp

110

115

120

125

tagagaccca agaaaacctg gaactttgga tcaatttctt tttcataggg gtggaacttg 447

cacagcaaaa acaaacaaac gcaagaagag atttgggctt taacacactg ggtactttgt 507

gggtctctct ttcgtcgggtg gcttaaagta acatctatct ccattgatcc taggttcttc 567

ctgactgctt tctccaactg ttcacagcaa atgcttggat tttatgcagt aggcatctact 627

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ttcagtgaag aggacaaata gtttatttaa agcatttgtt ccaataagat aaatagaggg 747

aaacttggat gctaaaatta catgaatagg aatcttcctg gcacttagtg tttctatgtt 807

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attaaaaaca aggggggtgg gtaataaatg tatataacat taaataatgt aacgtaggtg 1347

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attggtgtag aaatgtgtga tttgggtggg cttttacatc ttgcctacca ttgcatgaaa 1467

cattgggggtt tcttcaaaat gtgtgtgtca tacttctttt gggagggggg ttgttttctt 1527

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ataaaatttc ctgaccaaatt tgttttgtgg aaatagatgt gtttgcaatt tgaagatatc 1707

tttctgtcca gaaggcaaaa ttaccgaatg ccatttttaa aagtatgcta taaactatgc 1767

tactctcata caggggaccc atatittaaa atctccagag ttgcttacat ctagattatc 1827

cagcacaatc ataaagtga tgacaaaccc tttgaatgaa attgtggcac aaaatctgtt 1887

caggttggtg taccgtgtaa agtggggatg gggtaaaagt ggtaaacgta ctgttgatc 1947

aacaaataaa gggtacagtt ttgtaagag 1976

<210> 158

<211> 125

<212> PRT

<213> Homo sapiens

<400> 158

Met Tyr Phe Ile Phe Thr Ser Phe Trp Ala Tyr Lys Ile Tyr Tyr Val

1 5 10 15

Tyr Gly Phe Met Met Leu Val Leu Val Ile Leu Cys Ile Val Thr Val

20 25 30

Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala Glu Asp Tyr

35 40 45

Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr Ala Ile Tyr

50 55 60

Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr Lys Met Tyr
65 70 75 80

Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala Val Phe Ser
85 90 95

Thr Ala Leu Gly Ile Met Cys Gly Ala Ile Gly Tyr Met Gly Thr Ser
100 105 110

Ala Phe Val Arg Lys Ile Tyr Thr Asn Val Lys Ile Asp
115 120 125

<210> 159

<211> 2067

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (208)..(948)

<400> 159

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ccacccccacg cggactcccc agctggcgcg cccctcccat ttgcctgtcc tggtcaggcc 180

cccacccacc ttcccacctg accagcc atg ggg gct gcg gtg ttt tgc ggc tgc 234

Met Gly Ala Ala Val Phe Cys Gly Cys

1

5

act ttc gtc gcg ttc ggc ccg gcc ttc gcg ctt ttc ttg atc act gtg 282

Thr Phe Val Ala Phe Gly Pro Ala Phe Ala Leu Phe Leu Ile Thr Val

10

15

20

25

gct ggg gac ccg ctt cgc gtt atc atc ctg gtc gca ggg gca ttt ttc 330

Ala Gly Asp Pro Leu Arg Val Ile Ile Leu Val Ala Gly Ala Phe Phe

30

35

40

tgg ctg gtc tcc ctg ctc ctg gcc tct gtg gtc tgg ttc atc ttg gtc 378

Trp Leu Val Ser Leu Leu Leu Ala Ser Val Val Trp Phe Ile Leu Val

45

50

55

cat gtg acc gac cgg tca gat gcc cgg ctc cag tac ggc ctc ctg att 426

His Val Thr Asp Arg Ser Asp Ala Arg Leu Gln Tyr Gly Leu Leu Ile

60

65

70

ttt ggt gct gct gtc tct gtc ctt cta cag gag gtg ttc cgc ttt gcc 474

Phe Gly Ala Ala Val Ser Val Leu Leu Gln Glu Val Phe Arg Phe Ala

75

80

85

tac tac aag ctg ctt aag aag gca gat gag ggg tta gca tcg ctg agt 522

Tyr Tyr Lys Leu Leu Lys Lys Ala Asp Glu Gly Leu Ala Ser Leu Ser

90

95

100

105

gag gac gga aga tca ccc atc tcc atc cgc cag atg gcc tat gtt tct 570

Glu Asp Gly Arg Ser Pro Ile Ser Ile Arg Gln Met Ala Tyr Val Ser

110

115

120

ggt ctc tcc ttc ggt atc atc agt ggt gtc ttc tct gtt atc agt att 618

Gly Leu Ser Phe Gly Ile Ile Ser Gly Val Phe Ser Val Ile Ser Ile

125

130

135

ttg gct gat gca ctt ggg cca ggt gtg gtt ggg atc cat gga gac tca 666

Leu Ala Asp Ala Leu Gly Pro Gly Val Val Gly Ile His Gly Asp Ser

140

145

150

ccc tat tac ttc ctg act tca gcc ttt ctg aca gca gcc att atc ctg 714

Pro Tyr Tyr Phe Leu Thr Ser Ala Phe Leu Thr Ala Ala Ile Ile Leu

155

160

165

ctc cat acc ttt tgg gga gtt gtg ttc ttt gat gcc tgt gag agg aga 762

Leu His Thr Phe Trp Gly Val Val Phe Phe Asp Ala Cys Glu Arg Arg

170

175

180

185

cgg tac tgg gct ttg ggc ctg gtg gtt ggg agt cac cta ctg aca tcg 810

Arg Tyr Trp Ala Leu Gly Leu Val Val Gly Ser His Leu Leu Thr Ser

190

195

200

gga ctg aca ttc ctg aac ccc tgg tat gag gcc agc ctg ctg ccc atc 858

Gly Leu Thr Phe Leu Asn Pro Trp Tyr Glu Ala Ser Leu Leu Pro Ile

205

210

215

tat gca gtc act gtt tcc atg ggg ctc tgg gcc ttc atc aca gct gga 906

Tyr Ala Val Thr Val Ser Met Gly Leu Trp Ala Phe Ile Thr Ala Gly

220

225

230

ggg tcc ctc cga agt att cag cgc agc ctc ttg tgt aag gac

948

Gly Ser Leu Arg Ser Ile Gln Arg Ser Leu Leu Cys Lys Asp

235

240

245

tgactacctg gactgatcgc ctgacagatc ccacctgcct gtccactgcc catgactgag 1008

cccagcccca gcccggtcc attgccctca ttctctgtct cttctcgtc ggtctacccc 1068

gctacctcca gggttttgct ttgtcctttt gtgaccgtta gtctctaagc tttaccagga 1128

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gctgtgggtga gctggccact ccagagctgc agtgccactg gaggagtcag actaccatga 1908

catcgtaggg aaggagggga gatttttttg tagtttttaa ttgggatgtg ggaggggchg 1968

ggaggttttc tataaactgt atcattttct gctgagggtg gagtgcacca tccttttaat 2028

caaggtgatt gtgattttga ctaataaaaa agaatttgt 2067

<210> 160

<211> 247

<212> PRT

<213> Homo sapiens

<400> 160

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1

5

10

15

Ala Phe Ala Leu Phe Leu Ile Thr Val Ala Gly Asp Pro Leu Arg Val

20

25

30

Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Leu
35 40 45

Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp
50 55 60

Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val
65 70 75 80

Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Lys
85 90 95

Ala Asp Glu Gly Leu Ala Ser Leu Ser Glu Asp Gly Arg Ser Pro Ile
100 105 110

Ser Ile Arg Gln Met Ala Tyr Val Ser Gly Leu Ser Phe Gly Ile Ile
115 120 125

Ser Gly Val Phe Ser Val Ile Ser Ile Leu Ala Asp Ala Leu Gly Pro
130 135 140

Gly Val Val Gly Ile His Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser
145 150 155 160

Ala Phe Leu Thr Ala Ala Ile Ile Leu Leu His Thr Phe Trp Gly Val
165 170 175

Val Phe Phe Asp Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu Gly Leu
180 185 190

Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro

195

200

205

Trp Tyr Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met

210

215

220

Gly Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln

225

230

235

240

Arg Ser Leu Leu Cys Lys Asp

245

<210> 161

<211> 2807

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (264)..(1301)

<400> 161

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cagtgtttta aaactcaact ttcaaagaaa agatagtatt gctccctggt tcattaaaac 180

ctagagagat gtaatcagta agcaagaagg aaaaagggaa attcacaaag taactttttg 240

tgtctgtttc tttttaaccc agc atg gag aga aaa ttt atg tcc ttg caa cca 293

Met Glu Arg Lys Phe Met Ser Leu Gln Pro

1

5

10

tcc atc tcc gta tca gaa atg gaa cca aat ggc acc ttc agc aat aac 341

Ser Ile Ser Val Ser Glu Met Glu Pro Asn Gly Thr Phe Ser Asn Asn

15

20

25

aac agc agg aac tgc aca att gaa aac ttc aag aga gaa ttt ttc cca 389

Asn Ser Arg Asn Cys Thr Ile Glu Asn Phe Lys Arg Glu Phe Phe Pro

30

35

40

att gta tat ctg ata ata ttt ttc tgg gga gtc ttg gga aat ggg ttg 437

Ile Val Tyr Leu Ile Ile Phe Phe Trp Gly Val Leu Gly Asn Gly Leu

45

50

55

tcc ata tat gtt ttc ctg cag cct tat aag aag tcc aca tct gtg aac 485

Ser Ile Tyr Val Phe Leu Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn

60

65

70

gtt ttc atg cta aat ctg gcc att tca gat ctc ctg ttc ata agc acg 533

Val Phe Met Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr

75

80

85

90

ctt ccc ttc agg gct gac tat tat ctt aga ggc tcc aat tgg ata ttt 581

Leu Pro Phe Arg Ala Asp Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe

95	100	105	
gga gac ctg gcc tgc agg att atg tct tat tcc ttg tat gtc aac atg			629
Gly Asp Leu Ala Cys Arg Ile Met Ser Tyr Ser Leu Tyr Val Asn Met			
110	115	120	

tac agc agt att tat ttc ctg acc gtg ctg agt gtt gtg cgt ttc ctg			677
Tyr Ser Ser Ile Tyr Phe Leu Thr Val Leu Ser Val Val Arg Phe Leu			
125	130	135	

gca atg gtt cac ccc ttt cgg ctt ctg cat gtc acc agc atc agg agt			725
Ala Met Val His Pro Phe Arg Leu Leu His Val Thr Ser Ile Arg Ser			
140	145	150	

gcc tgg atc ctc tgt ggg atc ata tgg atc ctt atc atg gct tcc tca			773
Ala Trp Ile Leu Cys Gly Ile Ile Trp Ile Leu Ile Met Ala Ser Ser			
155	160	165	170

ata atg ctc ctg gac agt ggc tct gag cag aac ggc agt gtc aca tca			821
Ile Met Leu Leu Asp Ser Gly Ser Glu Gln Asn Gly Ser Val Thr Ser			
175	180	185	

tgc tta gag ctg aat ctc tat aaa att gct aag ctg cag acc atg aac			869
Cys Leu Glu Leu Asn Leu Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn			
190	195	200	

tat att gcc ttg gtg gtg ggc tgc ctg ctg cca ttt ttc aca ctc agc			917
Tyr Ile Ala Leu Val Val Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser			
205	210	215	

atc tgt tat ctg ctg atc att cgg gtt ctg tta aaa gtg gag gtc cca 965

Ile Cys Tyr Leu Leu Ile Ile Arg Val Leu Leu Lys Val Glu Val Pro

220

225

230

gaa tcg ggg ctg cgg gtt tct cac agg aag gca ctg acc acc atc atc 1013

Glu Ser Gly Leu Arg Val Ser His Arg Lys Ala Leu Thr Thr Ile Ile

235

240

245

250

atc acc ttg atc atc ttc ttc ttg tgt ttc ctg ccc tat cac aca ctg 1061

Ile Thr Leu Ile Ile Phe Phe Leu Cys Phe Leu Pro Tyr His Thr Leu

255

260

265

agg acc gtc cac ttg acg aca tgg aaa gtg ggt tta tgc aaa gac aga 1109

Arg Thr Val His Leu Thr Thr Trp Lys Val Gly Leu Cys Lys Asp Arg

270

275

280

ctg cat aaa gct ttg gtt atc aca ctg gcc ttg gca gca gcc aat gcc 1157

Leu His Lys Ala Leu Val Ile Thr Leu Ala Leu Ala Ala Ala Asn Ala

285

290

295

tgc ttc aat cct ctg ctc tat tac ttt gct ggg gag aat ttt aag gac 1205

Cys Phe Asn Pro Leu Leu Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp

300

305

310

aga cta aag tct gca ctc aga aaa ggc cat cca cag aag gca aag aca 1253

Arg Leu Lys Ser Ala Leu Arg Lys Gly His Pro Gln Lys Ala Lys Thr

315

320

325

330

aag tgt gtt ttc cct gtt agt gtg tgg ttg aga aag gaa aca aga gta 1301

Lys Cys Val Phe Pro Val Ser Val Trp Leu Arg Lys Glu Thr Arg Val

335

340

345

taaggagctc ttagatgaga cctgttcttg tatccttgtg tccatcttca ttcactcata 1361

gtctccaaat gactttgtat ttacatcact cccaacaaat gttgattctt aatatttagt 1421

tgaccattac ttttgtaat aagacctact tcaaaaattt tattcagtgt attttcagtt 1481

gttgagtctt aatgagggat acaggaggaa aaatccctac tagagtcctg tgggctgaaa 1541

tatcagactg ggaaaaaatg caaagcacat tggatcctac ttttcttcag atattgaacc 1601

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ccccagagca gaaaagaagc acatcctaag attcagggaa agactaactg tgaaaaggaa 1781

ggctgtccta taacaaagca gcatcaagtc ccaagtaagg acagtgagag aaaaggggga 1841

gaaggattgg agcaaaaagag aactggcaat aagtagggga aggaagaatt tcattttgca 1901

ttgggagaga ggttctaaca cactgaaggc aaccctattt ctactgtttc tctcttgcca 1961

gggtattagg aaggacagga aaagtaggag gaggatctgg ggcattgccc taggaaatga 2021

aagaattgtg tatagaatgg aagggggatc atcaaggaca tgtatctcaa attttctttg 2081

agatgcaggt tagttgacct tgctgcagtt ctccctccca ttaattcatt gggatggaag 2141

ccaaaaataa aagaggtgcc tctgaggatt agggttgagc actcaaggga aagatggagt 2201

agagggcaaa tagcaaaagt tgttgactc ctgaaattct attaacattt ccgcagaaga 2261

tgagtaggga gatgctgcct tcccttttga gatagtgtag aaaaacacta gatagtgtga 2321

gaggttcctt tctgtccatt gaaacaaggc taaggatact accaactact atcaccatga 2381

ccattgtact gacaacaatt gaatgcagtc tccctgcagg gcagattatg ccaggcactt 2441

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ctaaac 2807

<211> 346

<212> PRT

<213> Homo sapiens

<400> 162

Met Glu Arg Lys Phe Met Ser Leu Gln Pro Ser Ile Ser Val Ser Glu

1 5 10 15

Met Glu Pro Asn Gly Thr Phe Ser Asn Asn Asn Ser Arg Asn Cys Thr

20 25 30

Ile Glu Asn Phe Lys Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile

35 40 45

Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu

50 55 60

Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu

65 70 75 80

Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp

85 90 95

Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg

100 105 110

Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe

115 120 125

Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe
130 135 140

Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly
145 150 155 160

Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser
165 170 175

Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu
180 185 190

Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val
195 200 205

Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile
210 215 220

Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val
225 230 235 240

Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe
245 250 255

Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr
260 265 270

Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val
275 280 285

Ile Thr Leu Ala Leu Ala Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu
 290 295 300

Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu
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Ser Val Trp Leu Arg Lys Glu Thr Arg Val
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<400> 163

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gagtgagctg cgccgcaccg tgccgtccca cccggcaccc accagtccg atg ggg ccg 178

Met Gly Pro

1

cag cgg cgg ctg tcc cct gcc ggg gcc gcc cta ctc tgg ggc ttc ctg 226
Gln Arg Arg Leu Ser Pro Ala Gly Ala Ala Leu Leu Trp Gly Phe Leu
5 10 15

ctc cag ctg aca gcc gct cag gaa gca atc ttg cat gcg tct gga aat 274
Leu Gln Leu Thr Ala Ala Gln Glu Ala Ile Leu His Ala Ser Gly Asn
20 25 30 35

ggc aca acc aag gac tac tgc atg ctt tat aac cct tat tgg aca gct 322
Gly Thr Thr Lys Asp Tyr Cys Met Leu Tyr Asn Pro Tyr Trp Thr Ala
40 45 50

ctt cca agt acc cta gaa aat gca act tcc att agt ttg atg aat ctg 370
Leu Pro Ser Thr Leu Glu Asn Ala Thr Ser Ile Ser Leu Met Asn Leu
55 60 65

act tcc aca cca cta tgc aac ctt tct gat att cct cct gtt ggc ata 418
Thr Ser Thr Pro Leu Cys Asn Leu Ser Asp Ile Pro Pro Val Gly Ile
70 75 80

aag agc aaa gca gtt gtg gtt cca tgg gga agc tgc cat ttt ctt gaa 466
Lys Ser Lys Ala Val Val Val Pro Trp Gly Ser Cys His Phe Leu Glu
85 90 95

aaa gcc aga att gca cag aaa gga ggt gct gaa gca atg tta gtt gtc 514
Lys Ala Arg Ile Ala Gln Lys Gly Gly Ala Glu Ala Met Leu Val Val

100	105	110	115	
aat aac agt gtc cta ttt cct ccc tca ggt aac aga tct gaa ttt cct				562
Asn Asn Ser Val Leu Phe Pro Pro Ser Gly Asn Arg Ser Glu Phe Pro				
	120	125	130	
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gat gtg aaa ata ctg att gca ttt ata agc tac aaa gac ttt aga gat				610
Asp Val Lys Ile Leu Ile Ala Phe Ile Ser Tyr Lys Asp Phe Arg Asp				
	135	140	145	
atg aac cag act cta gga gat aac att act gtg aaa atg tat tct cca				658
Met Asn Gln Thr Leu Gly Asp Asn Ile Thr Val Lys Met Tyr Ser Pro				
	150	155	160	
tcg tgg cct aac ttt gat tat act atg gtg gtt att ttt gta att gcg				706
Ser Trp Pro Asn Phe Asp Tyr Thr Met Val Val Ile Phe Val Ile Ala				
	165	170	175	
gtg ttc act gtg gca tta ggt gga tac tgg agt gga cta gtt gaa ttg				754
Val Phe Thr Val Ala Leu Gly Gly Tyr Trp Ser Gly Leu Val Glu Leu				
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gaa aac ttg aaa gca gtg aca act gaa gat aga gaa atg agg aaa aag				802
Glu Asn Leu Lys Ala Val Thr Thr Glu Asp Arg Glu Met Arg Lys Lys				
	200	205	210	
aag gaa gaa tat tta act ttt agt cct ctt aca gtt gta ata ttt gtg				850
Lys Glu Glu Tyr Leu Thr Phe Ser Pro Leu Thr Val Val Ile Phe Val				
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Val Ile Cys Cys Val Met Met Val Leu Leu Tyr Phe Phe Tyr Lys Trp

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ttg gtt tat gtt atg ata gca att ttc tgc ata gca tca gca atg agt 946

Leu Val Tyr Val Met Ile Ala Ile Phe Cys Ile Ala Ser Ala Met Ser

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ctg tac aac tgt ctt gct gca cta att cat aag aca cca tat gga caa 994

Leu Tyr Asn Cys Leu Ala Ala Leu Ile His Lys Thr Pro Tyr Gly Gln

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tgc acg att gca tgt cgt ggc aaa aac atg gaa gtg aga ctt att ttt 1042

Cys Thr Ile Ala Cys Arg Gly Lys Asn Met Glu Val Arg Leu Ile Phe

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ctc tct gga ctg tgc ata gca gta gct gtt gtt tgg gct gtg ttt cga 1090

Leu Ser Gly Leu Cys Ile Ala Val Ala Val Val Trp Ala Val Phe Arg

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Asn Glu Asp Arg Trp Ala Trp Ile Leu Gln Asp Ile Leu Gly Ile Ala

310

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Phe Cys Leu Asn Leu Ile Lys Thr Leu Lys Leu Pro Asn Phe Lys Ser

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tgt gtg ata ctt cta ggc ctt ctc ctc ctc tat gat gta ttt ttt gtt 1234

Cys Val Ile Leu Leu Gly Leu Leu Leu Leu Tyr Asp Val Phe Phe Val

340 345 350 355

ttc ata aca cca ttc atc aca aag aat ggt gag agt atc atg gtt gaa 1282

Phe Ile Thr Pro Phe Ile Thr Lys Asn Gly Glu Ser Ile Met Val Glu

360 365 370

ctc gca gct gga cct ttt gga aat aat gaa aag ttg cca gta gtc atc 1330

Leu Ala Ala Gly Pro Phe Gly Asn Asn Glu Lys Leu Pro Val Val Ile

375 380 385

aga gta cca aaa ctg atc tat ttc tca gta atg agt gtg tgc ctc atg 1378

Arg Val Pro Lys Leu Ile Tyr Phe Ser Val Met Ser Val Cys Leu Met

390 395 400

cct gtt tta ata ttg ggt ttt gga gac att att gta cca ggc ctg ttg 1426

Pro Val Leu Ile Leu Gly Phe Gly Asp Ile Ile Val Pro Gly Leu Leu

405 410 415

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420 425 430 435

tac tat gtt tcg tct aca gtt gcc tat gct ttt ggc atg ata ctt aca 1522

Tyr Tyr Val Ser Ser Thr Val Ala Tyr Ala Phe Gly Met Ile Leu Thr

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Phe Val Val Leu Val Leu Met Lys Lys Gly Gln Pro Ala Leu Leu Tyr

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Leu Val Pro Cys Thr Leu Ile Thr Ala Ser Val Val Ala Trp Arg Arg

470

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aag gaa atg aaa aag ttc tgg aaa ggt aac agc tat cag atg atg gac 1666

Lys Glu Met Lys Lys Phe Trp Lys Gly Asn Ser Tyr Gln Met Met Asp

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cat ttg gat tgt gca aca aat gaa gaa aac cct gtg ata tct ggt gaa 1714

His Leu Asp Cys Ala Thr Asn Glu Glu Asn Pro Val Ile Ser Gly Glu

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cag att gtc cag caa taatattatg tggaactgct ataatgtgtc attgattttc 1769

Gln Ile Val Gln Gln

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1964

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<212> PRT

<213> Homo sapiens

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Ser Gly Asn Gly Thr Thr Lys Asp Tyr Cys Met Leu Tyr Asn Pro Tyr

35 40 45

Trp Thr Ala Leu Pro Ser Thr Leu Glu Asn Ala Thr Ser Ile Ser Leu

50 55 60

Met Asn Leu Thr Ser Thr Pro Leu Cys Asn Leu Ser Asp Ile Pro Pro

65 70 75 80

Val Gly Ile Lys Ser Lys Ala Val Val Val Pro Trp Gly Ser Cys His

85 90 95

Phe Leu Glu Lys Ala Arg Ile Ala Gln Lys Gly Gly Ala Glu Ala Met

100 105 110

Leu Val Val Asn Asn Ser Val Leu Phe Pro Pro Ser Gly Asn Arg Ser

115 120 125

Glu Phe Pro Asp Val Lys Ile Leu Ile Ala Phe Ile Ser Tyr Lys Asp

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135

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Phe Arg Asp Met Asn Gln Thr Leu Gly Asp Asn Ile Thr Val Lys Met

145

150

155

160

Tyr Ser Pro Ser Trp Pro Asn Phe Asp Tyr Thr Met Val Val Ile Phe

165

170

175

Val Ile Ala Val Phe Thr Val Ala Leu Gly Gly Tyr Trp Ser Gly Leu

180

185

190

Val Glu Leu Glu Asn Leu Lys Ala Val Thr Thr Glu Asp Arg Glu Met

195

200

205

Arg Lys Lys Lys Glu Glu Tyr Leu Thr Phe Ser Pro Leu Thr Val Val

210

215

220

Ile Phe Val Val Ile Cys Cys Val Met Met Val Leu Leu Tyr Phe Phe

225

230

235

240

Tyr Lys Trp Leu Val Tyr Val Met Ile Ala Ile Phe Cys Ile Ala Ser

245

250

255

Ala Met Ser Leu Tyr Asn Cys Leu Ala Ala Leu Ile His Lys Thr Pro

260

265

270

Tyr Gly Gln Cys Thr Ile Ala Cys Arg Gly Lys Asn Met Glu Val Arg

275

280

285

Leu Ile Phe Leu Ser Gly Leu Cys Ile Ala Val Ala Val Val Trp Ala
 290 295 300

Val Phe Arg Asn Glu Asp Arg Trp Ala Trp Ile Leu Gln Asp Ile Leu
 305 310 315 320

Gly Ile Ala Phe Cys Leu Asn Leu Ile Lys Thr Leu Lys Leu Pro Asn
 325 330 335

Phe Lys Ser Cys Val Ile Leu Leu Gly Leu Leu Leu Leu Tyr Asp Val
 340 345 350

Phe Phe Val Phe Ile Thr Pro Phe Ile Thr Lys Asn Gly Glu Ser Ile
 355 360 365

Met Val Glu Leu Ala Ala Gly Pro Phe Gly Asn Asn Glu Lys Leu Pro
 370 375 380

Val Val Ile Arg Val Pro Lys Leu Ile Tyr Phe Ser Val Met Ser Val
 385 390 395 400

Cys Leu Met Pro Val Leu Ile Leu Gly Phe Gly Asp Ile Ile Val Pro
 405 410 415

Gly Leu Leu Ile Ala Tyr Cys Arg Arg Phe Asp Val Gln Thr Gly Ser
 420 425 430

Ser Tyr Ile Tyr Tyr Val Ser Ser Thr Val Ala Tyr Ala Phe Gly Met

435

440

445

Ile Leu Thr Phe Val Val Leu Val Leu Met Lys Lys Gly Gln Pro Ala

450

455

460

Leu Leu Tyr Leu Val Pro Cys Thr Leu Ile Thr Ala Ser Val Val Ala

465

470

475

480

Trp Arg Arg Lys Glu Met Lys Lys Phe Trp Lys Gly Asn Ser Tyr Gln

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Met Asp Ala Arg Trp Trp Ala Val

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gtg gtg ctg gct gcg ttc ccc tcc cta ggg gca ggt ggg gag act ccc 162

Val Val Leu Ala Ala Phe Pro Ser Leu Gly Ala Gly Gly Glu Thr Pro

10

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gaa gcc cct ccg gag tca tgg acc cag cta tgg ttc ttc cga ttt gtg 210

Glu Ala Pro Pro Glu Ser Trp Thr Gln Leu Trp Phe Phe Arg Phe Val

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Val Asn Ala Ala Gly Tyr Ala Ser Phe Met Val Pro Gly Tyr Leu Leu

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Val Gln Tyr Phe Arg Arg Lys Asn Tyr Leu Glu Thr Gly Arg Gly Leu

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tgc ttt ccc ctg gtg aaa gct tgt gtg ttt ggc aat gag ccc aag gcc 354

Cys Phe Pro Leu Val Lys Ala Cys Val Phe Gly Asn Glu Pro Lys Ala

75

80

85

tct gat gag gtt ccc ctg gcg ccc cga aca gag gcg gca gag acc acc 402

Ser Asp Glu Val Pro Leu Ala Pro Arg Thr Glu Ala Ala Glu Thr Thr

90

95

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ccg atg tgg cag gcc ctg aag ctg ctc ttc tgt gcc aca ggg ctc cag 450

Pro Met Trp Gln Ala Leu Lys Leu Leu Phe Cys Ala Thr Gly Leu Gln

105 110 115 120

gtg tct tat ctg act tgg ggt gtg ctg cag gaa aga gtg atg acc cgc 498

Val Ser Tyr Leu Thr Trp Gly Val Leu Gln Glu Arg Val Met Thr Arg

125 130 135

agc tat ggg gcc aca gcc aca tca ccg ggt gag cgc ttt acg gac tcg 546

Ser Tyr Gly Ala Thr Ala Thr Ser Pro Gly Glu Arg Phe Thr Asp Ser

140 145 150

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Gln Phe Leu Val Leu Met Asn Arg Val Leu Ala Leu Ile Val Ala Gly

155 160 165

ctc tcc tgt gtt ctc tgc aag cag ccc cgg cat ggg gca ccc atg tac 642

Leu Ser Cys Val Leu Cys Lys Gln Pro Arg His Gly Ala Pro Met Tyr

170 175 180

cgg tac tcc ttt gcc agc ctg tcc aat gtg ctt agc agc tgg tgc caa 690

Arg Tyr Ser Phe Ala Ser Leu Ser Asn Val Leu Ser Ser Trp Cys Gln

185 190 195 200

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Tyr Glu Ala Leu Lys Phe Val Ser Phe Pro Thr Gln Val Leu Ala Lys

205 210 215

gcc tct aag gtg atc cct gtc atg ctg atg gga aag ctt gtg tct cgg 786

Ala Ser Lys Val Ile Pro Val Met Leu Met Gly Lys Leu Val Ser Arg

220

225

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cgc agc tac gaa cac tgg gag tac ctg aca gcc acc ctc atc tcc att 834

Arg Ser Tyr Glu His Trp Glu Tyr Leu Thr Ala Thr Leu Ile Ser Ile

235

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Gly Val Ser Met Phe Leu Leu Ser Ser Gly Pro Glu Pro Arg Ser Ser

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255

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Pro Ala Thr Thr Leu Ser Gly Leu Ile Leu Leu Ala Gly Tyr Ile Ala

265

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Phe Asp Ser Phe Thr Ser Asn Trp Gln Asp Ala Leu Phe Ala Tyr Lys

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Met Ser Ser Val Gln Met Met Phe Gly Val Asn Phe Phe Ser Cys Leu

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ttc aca gtg ggc tca ctg cta gaa cag ggg gcc cta ctg gag gga acc 1074

Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr

315

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cgc ttc atg ggg cga cac agt ggg ttt gct gcc cat gcc ctg cta ctc 1122

Arg Phe Met Gly Arg His Ser Gly Phe Ala Ala His Ala Leu Leu Leu

330	335	340	
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Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly			
345	350	355	360

cag ttt ggg gct gcc gtc ttc acc atc atc atg acc ctc cgc cag gcc	1218		
Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala			
365	370	375	

ttt gcc atc ctt ctt tcc tgc ctt ctc tat ggc cac act gtc act gtg	1266		
Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val			
380	385	390	

gtg gga ggg ctg ggg gtg gct gtg gtc ttt gct gcc ctc ctg ctc aga	1314		
Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg			
395	400	405	

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Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro			
410	415	420	

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Val Glu Ser Pro Val Gln Lys Val			
425	430		

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